

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 15:38:38 ; Search time 53.39 Seconds
(without alignments)
667.816 Million cell updates/sec

Title: US-09-945-182-26
Perfect score: 1757
Sequence: 1 NSDSLHTPLRRQKYLFDVSM.....GNVVYKQYEDMWVESCGR 321

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
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21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1757	100.0	321	16	AA1980
2	1757	100.0	321	18	AA1981
3	1757	100.0	321	22	AA1982
4	1747	99.4	455	22	AA1983
5	1368	77.9	436	17	AA1984
6	1207.5	68.7	263	16	AA1985
7	1207.5	68.7	263	18	AA1986
8	1202.5	68.4	263	22	AA1987
9	771	43.9	401	14	AA1988
10	771	43.9	501	16	AA1989
11	771	43.9	501	18	AA1990

12	771	43.9	501	18	AA19210	Human TGF-beta pro
13	771	43.9	501	18	AA19190	Human high mol. wt
14	771	43.9	501	18	AA19199	Human MP52 protein
15	771	43.9	501	18	AA19270	Human bone morphog
16	771	43.9	501	19	AA19486	TGF-beta superfami
17	771	43.9	501	19	AA19300	Human MP52. Homo
18	765	43.5	388	16	AA19734	Human bone morphog
19	765	43.5	388	18	AA19652	Human bone morphog
20	765	43.5	388	22	AA19986	Human bone morphog
21	765	43.5	495	15	AA19022	Growth differentia
22	765	43.5	495	22	AA19450	Amino acid sequenc
23	762	43.4	501	17	AA19563	Cartilage-derived
24	762	43.4	501	17	AA19563	Human growth diffe
25	760	43.3	501	21	AA19203	Human TGF-beta MP5
26	731	41.6	134	16	AA19687	GDF-6. Mus sp. A
27	731	41.6	134	21	AA19286	Murine growth diff
28	691.5	39.4	294	16	AA19729	Human bone morphog
29	691.5	39.4	294	18	AA19659	Human bone morphog
30	691.5	39.4	294	22	AA19072	Human bone morphog
31	618	35.2	240	16	AA19738	Murine mvl protein
32	618	35.2	240	18	AA19654	Murine BMP-12 homo
33	618	35.2	240	22	AA19084	Murine partial mvl
34	601	34.2	184	22	AA19375	Novel human diagno
35	584	33.2	411	16	AA19740	Fusion of BMP-2 pr
36	584	33.2	411	18	AA19659	BMP-2 propeptide/B
37	584	33.2	411	22	AA19083	Human BMP2 propept
38	575	32.7	102	21	AA19554	Human CDMP-2/GDF-6
39	575	32.7	102	21	AA19280	Human CDMP-2/GDF-6
40	575	32.7	102	21	AA19257	CDMP-2/GDF-6 finge
41	572	32.6	102	21	AA19555	Murine GDF-6, SEQ
42	572	32.6	102	21	AA19281	Mouse GDF-6 amino
43	572	32.6	102	21	AA19258	GDF-6 finger-1-hee
44	563	32.0	102	21	AA19556	Bovine CDMP-2, SE
45	563	32.0	102	21	AA19282	Bovine CDMP-2 amin

ALIGNMENTS

RESULT 1

AA19730	AA19730	standard; Protein; 321 AA.
ID	AA19730	standard; Protein; 321 AA.
XX	AA19730	
AC	AA19730	
XX	AA19730	
DT	30-NOV-1995	(first entry)
XX	30-NOV-1995	
DE	Human mature VL-1 (BMP-13) encoding sequence.	
XX	Human mature VL-1 (BMP-13) encoding sequence.	
XX	Human mature VL-1 (BMP-13) encoding sequence.	
KW	Bone morphogenetic protein; VL-1; tendon; ligament; tendinitis.	
XX	Bone morphogenetic protein; VL-1; tendon; ligament; tendinitis.	
OS	Homo sapiens.	
XX	Homo sapiens.	
Key	Location/Qualifiers	
FT	Peptide 1..201	
FT	Protein 202..321	
FT	/label= mature protein	
FT	Misc-difference 202..321	
FT	/note= "claimed"	
FT	Misc-difference 220..321	
FT	/note= "claimed"	
XX	WO9516035-A.	
PN	WO9516035-A.	
XX	15-JUN-1995.	
XX	15-JUN-1995.	
XX	06-DEC-1994; 94WO-US14030.	
XX	06-DEC-1994; 94WO-US14030.	
PR	02-NOV-1994; 94US-0333576.	
PR	07-DEC-1993; 93US-0164103.	
PR	25-MAR-1994; 94US-0217780.	
XX	25-MAR-1994; 94US-0217780.	
PA	(GEMY) GENETICS INST INC.	

```

PA (HARD ) HARVARD COLLEGE.
XX
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
XX
XX WPI: 1995-224320/29.
DR N-PSDB; AAQ96208.
XX
XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
PT compsn. for inducing tendon/ligament-like tissue formation
XX
XX Claim 14; Page 62-64; 84pp; English.
XX
XX BMP-12 related proteins are a subset of the BMP/TGF-beta/Vg-1
CC family of proteins, including BMP-12 and Vg-1. Vg-1 is designated
CC BMP-13. Like BMP-12, it is expected that BMP-13, as expressed by
CC mammalian cells such as CHO cells, exists as a heterogeneous popn.
CC of active species of BMP-13 protein with varying N-termini. It is
CC expected that all active species will contain the AA sequence
CC beginning with the 19th Cys residue of the mature protein until
CC the 119th residue of the mature protein or until the stop codon
CC after the 120th residue of the mature protein. Other active
CC species contain additional AA sequence in the N-terminal direction.
CC AAQ96208 is a partial DNA sequence and AAR78730 is the derived AA
CC sequence of a portion of the 2.5 kb DNA insert of the plasmid
CC subclone pGEM1Dc31/2.5, derived from clone lambdaJLDc31.
XX
XX Sequence 321 AA;
SQ

Query Match 100.0%; Score 1757; DB 16; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.2e-149;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSDLSHTPLRRQKYLFDVSMLSDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCLS 60
Db 1 NSDLSHTPLRRQKYLFDVSMLSDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCLS 60

Qy 61 LLLDARTLDPOGAPAGWEVDFVWQGLRHQPWKQLCLELRAAANGELDAGEAARAGPQ 120
Db 61 LLLDARTLDPOGAPAGWEVDFVWQGLRHQPWKQLCLELRAAANGELDAGEAARAGPQ 120

Qy 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGS 180
Db 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGS 180

Qy 181 PPSGADARPLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKPLHVNFKELGWDWIIA 240
Db 181 PPSGADARPLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKPLHVNFKELGWDWIIA 240

Qy 241 PLEYEAYHCEGVCDPLRLSHLEPTNHALIOTLNMMDPGSTPPSCCVPTKITPISILY 300
Db 241 PLEYEAYHCEGVCDPLRLSHLEPTNHALIOTLNMMDPGSTPPSCCVPTKITPISILY 300

Qy 301 AGNNVYKQYEDVMVSCGCR 321
Db 301 AGNNVYKQYEDVMVSCGCR 321

RESULT 2
ID AAQ26591 standard; Protein; 321 AA.
XX
AC AAQ26591;
XX
DT 21-JAN-1998 (first entry)
XX
DE Human bone morphogenetic protein BMP-13.
XX
KW BMP-13; bone morphogenetic protein; human; tendon; ligament;
KW wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
KW therapy.
XX

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```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..201
XX Protein /label= sig_peptide
XX 202..321
XX /label= Mat_protein
XX /note= "Claim 5"
XX 218..294
XX /note= "Claim 5"
XX
XX US5658882-A.
XX
XX 19-AUG-1997.
XX
XX 07-DEC-1993; 93US-0164103.
XX
XX 22-DEC-1994; 94US-0362670.
XX 07-DEC-1993; 93US-0164103.
XX 25-MAR-1994; 94US-0217780.
XX 02-NOV-1994; 94US-0333576.
XX
XX (GEMY ) GENETICS INST INC.
XX (HARD ) HARVARD COLLEGE.
XX
XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
XX Wozney JM;
XX
XX WPI: 1997-424270/39.
XX N-PSDB; AAT90386.
XX
XX Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
XX - useful for tissue healing and repair, treatment of tendonitis,
XX improving fixation of tendons to bone etc
XX
XX Claim 5; Column 57-60; 43pp; English.
XX
XX This polypeptide comprises a novel bone morphogenetic protein,
XX designated BMP-13 that induces tendon and ligament formation. Its
XX amino acid sequence was deduced from isolated genomic clone vi-1
XX (see AAT90386). A claimed method for inducing formation of tendon
XX and/or ligament tissues involves the administration of a
XX composition containing at least one protein selected from BMP-13,
XX MP52 (see AAW26590) and BMP-12 (see AAW26589). The method is used for
XX tissue (including skin) healing and repair. This is useful for
XX treating tendonitis, carpal tunnel syndrome and other defects of
XX traumatic or congenital origin, in cosmetic surgery and to improve
XX fixation of tendons or ligaments to bone. The specified proteins
XX can also be used to increase activity of other BMPs e.g. BMP-2
XX (see AAW26597).
XX
XX Sequence 321 AA;
SQ

Query Match 100.0%; Score 1757; DB 18; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.2e-149;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSDLSHTPLRRQKYLFDVSMLSDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCLS 60
Db 1 NSDLSHTPLRRQKYLFDVSMLSDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCLS 60

Qy 61 LLLDARTLDPOGAPAGWEVDFVWQGLRHQPWKQLCLELRAAANGELDAGEAARAGPQ 120
Db 61 LLLDARTLDPOGAPAGWEVDFVWQGLRHQPWKQLCLELRAAANGELDAGEAARAGPQ 120

Qy 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGS 180
Db 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGS 180

Qy 181 PPSGADARPLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKPLHVNFKELGWDWIIA 240
Db 181 PPSGADARPLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKPLHVNFKELGWDWIIA 240

```

QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLMSMDPGSTPPSCCVPTKLTPISILYID 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 pleyeayhcegvcdplrshleptnhaiqltmsmdpgstppscvptkltpisilyid 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 AGNNVYKQYEDMVVESCGR 321
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 agnnvykyedmvvescgr 321
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3
 AAE10982
 ID AAE10982 standard; Protein: 321 AA.
 XX
 AC AAE10982;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 XX Human full length VL-1 or BMP-13 protein.
 XX
 XX Human: bone morphogenic protein; BMP-13; vulnerary; antiinflammatory;
 XX analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
 KW tissue formation; wound healing; tissue repair; ligament defect; VL-1;
 KW carpal tunnel syndrome; tendonitis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..201
 FT /label= Signal_peptide
 FT Protein 202..321
 FT /label= Mature_BMP_12_protein
 FT
 XX
 XX US6284872-B1.
 XX
 XX 04-SEP-2001.
 XX
 XX 28-FEB-1997; 97US-0808324.
 XX
 XX 22-DEC-1994; 94US-0362670.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX
 XX (GEMY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX
 XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 Melton DA;
 DR WPI: 2001-588978/66.
 DR N-PSDB; AAD18333.
 XX
 XX New chimeric DNAs, useful for treating tendonitis, carpal tunnel
 PT syndrome and other tendon and ligament defects, comprises DNA encoding
 PT propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
 PT BMP-13 or MP52 -
 XX
 XX Example 1; Column 57-60; 42pp; English.
 PS
 XX
 XX The invention relates to a chimeric DNA comprising a DNA sequence
 CC encoding a propeptide from a member of the transforming growth factor
 CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
 CC encoding an amino acid sequence encoding a mature polypeptide consisting
 CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
 CC sequences are useful for producing proteins which induce tendon/ligament
 CC like tissue formation, and for isolating and cloning further DNA
 CC sequences encoding BMP-12 related proteins with similar activity. The
 CC proteins are useful for the induction of tendon/ligament-like tissue
 CC formation, wound healing, ligament and other tissue repair, augmenting
 CC the activity of bone morphogenetic proteins, and for treating tendonitis,
 CC carpal tunnel syndrome and other tendon and ligament defects. The
 CC present sequence is human VL-1 protein also designated as BMP-13.

XX Sequence 321 AA;
 SQ
 Query Match 100.0%; Score 1757; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 8.2e-149;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NSDLSHTPLRROKYLEFDVSMLSKDEELVGAELRLFRQAPSPAGPPLHVQLFPCLSP 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 nsdlshtplrqrkyldvsmldskdelvgaelrlfrqapsapwppagplhvqlfclsp 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 LLLDARTLDPOGAPPAGWEVDFVMOGLRHQPWKQLCLELRAANGELDAGEAEARARGPQ 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 llldartldpogappagwevdfwqglrhqpwkqlclelraaageldageaeeararqpq 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 PPPPDLRSLGFRVRPPQERALLVFTSRQKNLFAEMREQLGSAEAGPGAGAGSGWP 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ppppdlrslgfrvrppqerallvftsrqknlfamreqlgsaeagpgagagswp 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 PPSGAPDARPLWSPGRRRRRTAFASRHGKRHCKSKPLHVNFKELGWDWIIA 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 ppsgapdarplwspgrrrrrtafasrhgkrhckskplhvnfkelnwddwila 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLMSMDPGSTPPSCCVPTKLTPISILYID 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 pleyeayhcegvcdplrshleptnhaiqltmsmdpgstppscvptkltpisilyid 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 4
 AAM50216
 ID AAM50216 standard; Protein: 455 AA.
 XX
 AC AAM50216;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 XX Human growth/differentiation factor-6-like protein AMF10.
 DE AMF10; human; growth/differentiation factor-6; cancer;
 KW cell proliferation; astrocytoma; glioma; therapy; diagnosis.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT Protein 23..455
 FT /label= Mature_protein
 FT
 XX
 XX WO200174897-A2.
 PN
 XX
 XX 11-OCT-2001.
 PD
 XX
 XX 03-APR-2001; 2001WO-US10892.
 PF
 XX
 XX 03-APR-2000; 2000US-194314P.
 PR 16-AUG-2000; 2000US-225693P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Vernet CAM, Burgess CE, Fernandes E, Taupier RJ, Quinn KE;
 PI Spytek KA, Rastelli L, Herrmann JL;
 XX
 XX WPI: 2001-626395/72.
 DR N-PSDB; AAI70203.
 DR
 XX
 XX New AMF1-10 polypeptides and encoding polynucleotides, useful for
 PT treating or preventing disorders related to modulation of cell

PT movement, cell signal processing, cell adhesion or migration pathways
PT e.g., cancer
XX
PS Claim 1: Page 44-45; 134pp; English.
XX
CC The present sequence is that of the novel, secreted human
CC growth/differentiation factor-6 (GDF6)-like protein, AMF10.
CC AMF10 is expressed in astrocytoma and glioma-derived tissue. DNA
CC encoding the AMF8 may be useful in gene therapy, and the protein
CC may also be used as a therapeutic, especially in treatment of
CC cancer and other cell proliferative disorders. Generally, the
CC AMF1-10 (AMFX) nucleic acids and proteins of the invention are useful
CC for treating or preventing AMFX-associated disorders, e.g. a disorder
CC related to cell signal processing and metabolic pathway modulation,
CC cell adhesion or migration pathway modulation, chemoresistance,
CC radiotherapy resistance, survival in trophic factor limited
CC secondary tissue site microenvironments, connective tissue
CC disorders, tissue remodeling, oncogenesis, cancer of the breast,
CC ovary, cervix, prostate, endometrium, stomach, colon, lung,
CC bladder, kidney, brain, and soft-tissue, cellular transformation,
CC developmental tissue remodeling, inflammation, blood clot
CC formation and resorption, haematopoiesis, angiogenesis, multidrug
CC resistance related to organic anion transporters, malignant disease
CC progression, autocrine and paracrine regulation of cell growth, and
CC cellular responses to external stimuli, and other diseases,
CC disorders, etc. (all claimed). AMFX proteins are also used for
CC screening drugs or compounds that modulate AMFX protein activity or
CC expression as well as to treat disorders characterized by
CC insufficient or excessive production of AMFX protein.
XX
SQ Sequence 455 AA;

Query Match 99.4%; Score 1747; DB 22; Length 455;
Best Local Similarity 100.0%; Pred. No. 9.8e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 DLSHTPLRRQKYLFDVSMLELVAELRFRQAPSAPWGPAGPLHVQLFPCLSPLL 62
Db 137 dlshtplrqqylfdvsmlelvaelrfrqapsapwgpagplhvqlfpcispll 196
Oy 63 LDARTLDPQAGPAGWEVDFVWGLRHQPWKQLCLLELAAMGELDAGEAEARAGPQQPP 122
Db 197 ldartldpqagpagwevdfvwwglrhqpwkqlcllelaaawgeldageaeatargpqqpp 256
Oy 123 PPDLRLSGFGRVRPPOERALLVVFTRSQKLNLFAMRQOLGSAEAGPAGAGSWPPP 182
Db 257 ppdlrlsfgfgrvrppqerallvvtfsqrknlfaemreqlgsaeagpagaegswppp 316
183 SGAPDARPLPSPGRRRRRTAFASRHGKRSKRLCSKKPLHVNFKELGWDWIIAPL 242
317 sgapdarplpspgrrrrrtafasrhgkrskrlcskkplhvnfkelgwdwiiapl 376
Oy 243 EYEAHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPIISILYIDAG 302
Db 377 eyeahcegvcdflrshleptnhaiiqtlmnsmdpgstppscvptkltipisilyidag 436
Oy 303 NNVVYKOYEDMVVSCGCR 321
Db 437 nnvvykyedmvvscgcr 455
RESULT 5
AAR95636
ID AAR95636 standard; Protein; 436 AA.
XX
AC AAR95636;
XX
DT 25-OCT-1996 (first entry)
XX
DE Cartilage-derived morphogenetic protein-2.
XX Cattle; cartilage-derived morphogenetic protein-2;
KW

KW articular cartilage; chondrogenic; vulnery; implantation;
KW chondromalacia; osteoarthritis; therapy; joint repair.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT Region 1..312
FT /note= "pro-region"
FT Modified-site 89..91
FT /note= "N-glycosylation site"
FT Cleavage-site 313..316
FT /note= "proteolytic processing site"
FT Domain 317..436
FT /note= "C-terminal mature domain"
FT Peptide 352..382
FT /note= "Consensus conserved motif (AAR95641)"
XX
PN WO9614335-A1.
XX
XX 17-MAY-1996.
PD
XX 07-NOV-1994; 94WO-US12814.
PF
XX 07-NOV-1994; 94WO-US12814.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Chang SC, Luyten FP, Moos M;
PI
XX WPI; 1996-251714/25.
DR N-PSDB; AAT31602.
XX
PT New purified cartilage extracts and proteins - used to stimulate the
PT development and repair of cartilage in vivo.
XX
PS Claim 11; Fig 2; 34pp; English.
XX
CC The sequence represents cattle articular cartilage-derived
CC morphogenetic protein-2 (CDMP-2). The N-terminal methionine and
CC signal peptide is missing, but part of the pro-region, a typical
CC proteolytic cleavage site and a C-terminal domain containing 7
CC highly conserved Cys residues characteristic of the transforming
CC growth factor-beta gene family are present. A single N-glycosylation
CC site is located in the pro-region. A consensus highly conserved
CC motif in CDMP proteins (AAR95641) is present in the C-terminal domain.
CC CDMP-2 is present in a purified cartilage extract (claimed) which
CC stimulates local cartilage formation and repair when combined with a
CC matrix and implanted in a mammal. The protein may be used in therapy
CC of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or
CC to repair cartilage after reconstructive surgery.
XX
SQ Sequence 436 AA;
Query Match 77.9%; Score 1368; DB 17; Length 436;
Best Local Similarity 81.7%; Pred. No. 6.6e-114;
Matches 268; Conservative 9; Mismatches 39; Indels 12; Gaps 6;
Oy 3 DLSHTPLRRQKYLFDVSMLELVAELRFRQAPSAPWGPAGPLHVQLFPCLSPLL 62
Db 112 dlshtplrqqylfdvsmlelvaelrfrqapsapwgpagplhvqlfpcispll 170
Oy 63 LDARTLDPQAGPAGWEVDFVWGLRHQPWKQLCLLELAAMGELDAGEAEARAGPQQPP 121
Db 171 gsaep-gpagaprgwvdfvwwglrhqpwkqlcllelaaawgelpgaedeartpgqqp 229
Oy 122 PPDLRLSGFGRVRPPOERALLVVFTRSQKLNLFAMRQOLGSAEAGPAGAGSW- 179
Db 230 ppdlrlsfgfgrvrppqerallvvtfsqrknlfaemreqlgsatevvgpggaegsgp 289
Oy 180 -----PPSPGAPDARPLPSPGRRRRRTAFASRHGKRSKRLCSKKPLHVNFKELG 233
Db 290 ppppppppsgtpdaglwspspg-rrrttafasrhgkrskrlcskkplhvnfkelg 348

```

QY 234 WDDWIIAPLEYAYHCEGVCDPLRSHLEPTNHAIQTLMNSMDPGSTPPSCVPTKLTLP 293
DB 349 WDDWIIAPLEYAYHCEGVCDPLRSHLEPTNHAIQTLMNSMDPGSTPPSCVPTKLTLP 408
QY 294 ISILYIDAGNNVYKQYEDMVYVESCGR 321
DB 409 ISILYIDAGNNVYKQYEDMVYVESCGR 436

RESULT 6
AAR78739
ID AAR78739 standard; Protein; 263 AA.
XX
AC AAR78739;
XX
DT 23-NOV-1995 (first entry)
XX
DE Murine mv2 protein..
XX
OS Bone morphogenetic protein; mv2; tendon; ligament.
XX
FH Mus musculus.
FT Key Location/Qualifiers
FT Misc-difference 54 /label= P,T
FT
XX
PN W09516035-A.
XX
PD 15-JUN-1995.
XX
PF 06-DEC-1994; 94WO-US14030.
XX
PR 02-NOV-1994; 94US-0333576.
XX
PR 07-DEC-1993; 93US-0164103.
XX
PR 25-MAR-1994; 94US-0217780.
XX
PA (GEM ) GENETICS INST INC.
PA (HARD ) HARVARD COLLEGE.
XX
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
XX
DR WPI: 1995-224320/29.
DR N-PSDB; AAQ96224.
XX
XX
XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
compn. for inducing tendon/ligament-like tissue formation
XX
XX Example; Page 71-72; 84pp; English.
XX
XX Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the
XX amplification of a 275 bp DNA probe, the internal 269 bp of which
XX corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding
XX plasmid subclone PCRI-142. This probe was radioactively labelled
XX and used to screen a murine genomic library. DNA sequence analysis
XX of one of positively hybridising recombinants named MVR32 indicates
XX that it encodes a portion of the mouse gene corresp. to the PCR
XX product mv2 (murine homolog of the human VL-1 sequence AAQ96213.
XX The partial DNA sequence of this subclone and corresp. AA
XX translation are given in AAQ96224 & AAR78739.
XX
SQ Sequence 263 AA;

Query Match 68.7%; Score 1207.5; DB 16; Length 263;
Best Local Similarity 83.7%; Pred. No. 7.9e-100;
Matches 231; Conservative 6; Mismatches 20; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLSPDLLDARTLDPQAGVEFVWQGLRHQPWKQLCIELEAAWGE 105
DB 7 pag-----ptlrgssgtqpr---pag-ksfdvwqglrqpqwkqlclelraawge 51

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```

QY 106 LDAGEAEARARGPOPPPPDLRSIGFGRYRPPPOERALLVVFTRSORKNLFAEMREOLGS 165
DB 52 LDxdtgarargppppppdlrsigfgrvrrppqerallvfrsqrknlfemheqlgs 111
QY 166 AEAAGPGAGARGSWPPSPGAPDARPWLPSPGRRRRRTAFASRHGKRHGKSRKSLRCSKKPL 225
DB 112 aea---agaegscpapspdtsqswlpqgrrrrrtafasrhgkrhgkksrlrcsrkpl 167
QY 226 HVNFKELGWDWIIAPLEYAYHCEGVCDPLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
DB 168 hvnfkelgwdwiiapleyayhcegvcdplrshleptnhaiqtlmnsmdpgstppsc 227
QY 286 CVPTKLTPISTILYIDAGNNVYKQYEDMVYVESCGR 321
DB 228 cvptkltpisillyidagnnvvykyedmvvescgr 263

RESULT 7
AAW26595
ID AAW26595 standard; Protein; 263 AA.
XX
AC AAW26595;
XX
DT 21-JAN-1998 (first entry)
XX
DE Murine BMP-13 homologue fragment.
XX
KW BMP-13; bone morphogenetic protein; mouse; tendon; ligament;
KW wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 54 /label= Pro, Thr
FT /note= "encoded by RCC"
FT Misc-difference 247 /note= "encoded by GTN"
FT
XX
XX US5658882-A.
XX
XX 19-AUG-1997.
XX
XX 07-DEC-1993; 93US-0164103.
XX
XX 22-DEC-1994; 94US-0362670.
XX 07-DEC-1993; 93US-0164103.
XX 25-MAR-1994; 94US-0217780.
XX 02-NOV-1994; 94US-0333576.
XX
XX (GEM ) GENETICS INST INC.
XX (HARD ) HARVARD COLLEGE.
XX
XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
XX Wozney JM;
XX
XX WPI: 1997-424270/39.
XX N-PSDB; AAT90397.
XX
XX Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
XX - useful for tissue healing and repair, treatment of tendonitis,
XX improving fixation of tendons to bone etc
XX
XX Example 1; Column 69-72; 43pp; English.
XX
XX This polypeptide comprises a fragment of a murine homologue of
XX human bone morphogenetic protein 12 (BMP-13) (see also AAW26591).
XX Its amino acid sequence was deduced from DNA subclone mv2 (see
XX AAT90397), isolated from murine genomic DNA using primers (see
XX AAT90393-94) based on human BMP-12 sequences. Human BMP-13, BMP-12
XX (see AAW26589) and MP52 (see AAW26590) polypeptides are used in a

```

CC claimed method for inducing tendon and ligament formation.

XX Sequence 263 AA;

Query Match 68.7%; Score 1207.5; DB 18; Length 263;
 Best Local Similarity 83.3%; Pred. No. 7.9e-100;
 Matches 231; Conservative 6; Mismatches 20; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLLDARTLDPOGAPPAGVEFVDMQGLRHQPKQLCLELRAAWGE 105
 Db 7 pag-----ptlrgssgtqpr---pag-ksfdvvgglrpgqwkqlclelraawge 51
 QY 106 LDAGEAARARGPQQPPDLRLSLGFGRRVRPPOERALLVVFTRSRQKQLFAEMRQOLGS 165
 Db 52 ldxgdtgarargpqppldlrslgfgrrvrppqerallvvftrsqrknlftemheqlgs 111
 QY 166 AEAAGPAGAGSGWPPSPGAPDARPLSPGRRRRRTAFASRHGKRHKKSLRCSKKPL 225
 Db 112 aea----agaegscpapspdgtgswlpsgrrrrrtafasrhgkngkksrlcsrkpl 167
 QY 226 HVNFKELGWDWIIAPLEYEAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
 Db 168 hvnfkelgwdwiiapleyeayhcegvcdflrshleptnhaiqltlnmsmdpgstppsc 227
 QY 286 CVPTKLTPTISILYIDAGNNVYKQYEDMVVESCGR 321
 Db 228 cvptkltptisilyidagnnvvykyedmvvescgr 263

RESULT 8

AAE10985
 ID AAE10985 standard; Protein; 263 AA.

XX AC AAE10985;

XX 18-DEC-2001 (first entry)

XX Murine partial mv2 protein.

XX Mouse; bone morphogenic protein; BMP-12; vulnery; antiinflammatory;
 KW analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
 KW tissue formation; wound healing; tissue repair; ligament defect;
 KW carpal tunnel syndrome; tendonitis; mv2.

XX Mus sp.

XX Key Location/Qualifiers
 FT Misc-difference 54 /label= Unknown

FT /note= "Encoded by RCC"

FT Misc-difference 247 /label= Unknown

FT /note= "Encoded by GTN"

XX US6284872-B1.

XX 04-SEP-2001.

XX 28-FEB-1997; 97US-0808324.

XX 22-DEC-1994; 94US-0362670.

XX 07-DEC-1993; 93US-0164103.

XX 25-MAR-1994; 94US-0217780.

XX 02-NOV-1994; 94US-0333576.

XX (GEMV) GENETICS INST INC.

XX (HARD) HARVARD COLLEGE.

XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;

XX PI Melton DA;

XX WPI; 2001-588978/66.

DR N-PSDB: AAD18336.

XX New chimeric DNAs, useful for treating tendonitis, carpal tunnel
 PT syndrome and other tendon and ligament defects, comprises DNA encoding
 PT propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
 PT BMP-13 or MP52 .

XX Example 1; Column 71-74; 42pp; English.

XX The invention relates to a chimeric DNA comprising a DNA sequence
 CC encoding a propeptide from a member of the transforming growth factor
 CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
 CC encoding an amino acid sequence encoding a mature polypeptide consisting
 CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
 CC sequences are useful for producing proteins which induce tendon/ligament
 CC like tissue formation, and for isolating and cloning further DNA
 CC sequences encoding BMP-12 related proteins with similar activity. The
 CC proteins are useful for the induction of tendon/ligament-like tissue
 CC formation, wound healing, ligament and other tissue repair, augmenting
 CC the activity of bone morphogenetic proteins, and for treating tendonitis,
 CC carpal tunnel syndrome and other tendon and ligament defects. The
 CC present sequence is murine partial mv2 protein which is homologous to
 CC human BMP-12 or VL-1 sequences of the invention.

XX Sequence 263 AA;

Query Match 68.4%; Score 1202.5; DB 22; Length 263;
 Best Local Similarity 83.3%; Pred. No. 2.2e-99;
 Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLLDARTLDPOGAPPAGVEFVDMQGLRHQPKQLCLELRAAWGE 105
 Db 7 pag-----ptlrgssgtqpr---pag-ksfdvvgglrpgqwkqlclelraawge 51
 QY 106 LDAGEAARARGPQQPPDLRLSLGFGRRVRPPOERALLVVFTRSRQKQLFAEMRQOLGS 165
 Db 52 ldxgdtgarargpqppldlrslgfgrrvrppqerallvvftrsqrknlftemheqlgs 111
 QY 166 AEAAGPAGAGSGWPPSPGAPDARPLSPGRRRRRTAFASRHGKRHKKSLRCSKKPL 225
 Db 112 aea----agaegscpapspdgtgswlpsgrrrrrtafasrhgkngkksrlcsrkpl 167
 QY 226 HVNFKELGWDWIIAPLEYEAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
 Db 168 hvnfkelgwdwiiapleyeayhcegvcdflrshleptnhaiqltlnmsmdpgstppsc 227
 QY 286 CVPTKLTPTISILYIDAGNNVYKQYEDMVVESCGR 321
 Db 228 cvptkltptisilyidagnnvvykyedmvvescgr 263

RESULT 9

AAR40800

ID AAR40800 standard; Protein; 401 AA.

XX AC AAR40800;

XX 11-FEB-1994 (first entry)

XX TGF-beta-like clone MP-52 protein.

XX Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
 KW bone; cartilage; tooth; wound repair; immunosuppressor;
 KW organ transplant; cosmetic surgery; antibody; diagnosis.

XX Homo sapiens.

XX WO9316099-A.

XX 19-AUG-1993.

XX 12-FEB-1993; 93WO-EP003350.

```
XX PR 12-FEB-1992; 92EP-0102324.
XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX PI Hoetten G, Neidhardt H;
XX DR WPI; 1993-272824/34.
XX DR N-PSDB; AAQ47709.
XX XX
XX PT New transforming growth factor-beta family proteins and DNA -
XX PT used in tissue and wound repair, in treatment of bone, cartilage
XX PT and tooth defects, and antibodies for diagnosis
XX XX
XX PS Claim 11; Page 19; 29pp; English.
XX XX
XX CC The sequences given in AAR40800 and AAR45447 represent fragments of
XX CC embryo and liver derived human transforming growth factor-beta
XX CC (TGF-beta) respectively. The full length protein may be used in a
XX CC pharmaceutical composition for the treatment of various bone, cartilage
XX CC or tooth defects and in tissue and wound repair processes. These
XX CC proteins may also be used as immunosuppressors in organ transplants and
XX CC in cosmetic surgery. Antibodies raised against these proteins may be
XX CC used for diagnostic purposes.
XX XX
XX SQ Sequence 401 AA;

Query Match 43.9%; Score 771; DB 14; Length 401;
Best Local Similarity 51.1%; Pred. No. 1.3e-60;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 9 LRROKYLFDVSMLSKDEELVCAELRLFRQAPS-----APWGPAGPLHVOLFCLSL--- 59
DB 117 VRKQYVFDISAL-ekdgligaelrlrkpsdtakpaapgggraaql--klsscpsgrq 173
QY 60 -PLLLDARTLDPQGAPPAGWEVDFVWQGLRH-OPWKQLCLELRAAWGELDAGEAEARAG 117
DB 174 PASLIDVRSV--pgldsgwvfdiwlfrnknsaqiclele-aw---ergra----- 221
QY 118 PQOPPPDLRLSGFGRVRRPQERALLVVFTRSORKNL-FAEMREQLGSAEAGPGAGAE 176
DB 222 -----vdlrglfgdraarqvhekalfivgrtkrdlffneikarsgddkt----- 268
QY 177 GSWPPPGAPDARPLSPGRRRTAFASRHGKRHKSKRLRCSKKPLHVNFKELGWDD 236
DB 269 -----vyeylfsq-rrkrraplratqgkrpsknkarscrkalhvnfdmgwdd 316
DB 237 WIAPLEYAYHCEGVGDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPISI 296
DB 317 WIAPLEYAEAFHCEGLCEFLPRLSHLEPTNHAVIQLMNSMDPESTPPTCCVPTRLSPISI 376
QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
DB 377 lfidsannvvykyedmvvescgr 401

RESULT 10
AAR69600
ID AAR69600 standard; Protein: 501 AA.
XX AC AAR69600;
XX DT 10-OCT-1995 (first entry)
XX DE New TGF-beta family member - MP-52 protein sequence.
XX KW Transforming growth factor-beta family; mitogenic; differentiation;
XX KW treatment; prevention; disease; bone; cartilage; connective tissue;
XX KW skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
XX KW tissue regeneration; arthritis; ss.
XX OS Homo sapiens.
```

```
XX XX
XX FT Peptide
XX FT 382
XX FT /label= mature protein
XX XX
XX PN WO9504819-A.
XX XX
XX PD 16-FEB-1995.
XX XX
XX PF 09-AUG-1994; 94WO-EP02630.
XX XX
XX PR 10-AUG-1993; 93DE-4326829.
XX PR 25-MAY-1994; 94DE-4418222.
XX PR 09-JUN-1994; 94DE-4420157.
XX XX
XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX XX
XX PI Hoetten G, Neidhardt H, Paulista M, Hoetten G;
XX XX
XX DR WPI; 1995-090897/12.
XX DR N-PSDB; AAQ83695.
XX XX
XX PT New DNA encoding a new member of the TGF beta family - and
XX PT related vectors, host cells etc., has mitogenic and
XX PT differentiation inducing activity, e.g. for treating or
XX PT preventing diseases of bone and cartilage etc.
XX XX
XX PS Claim 6; Page 36; 51pp; German.
XX XX
XX CC The amino acid sequence of a novel member of the transforming growth
XX CC factor-beta (TGF-b) family named MP-52. The gene encodes a protein
XX CC of 501 amino acids (AA). The protein, or at least the mature protein,
XX CC has mitogenic and/or differentiation inducing properties useful in
XX CC the treatment or prevention of diseases of bone, cartilage, connective
XX CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
XX CC be used for wound healing and tissue regeneration e.g. in osteoporosis
XX CC and arthritis.
XX XX
XX SQ Sequence 501 AA;

Query Match 43.9%; Score 771; DB 16; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.7e-60;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 9 LRROKYLFDVSMLSKDEELVCAELRLFRQAPS-----APWGPAGPLHVOLFCLSL--- 59
DB 217 VRKQYVFDISAL-ekdgligaelrlrkpsdtakpaapgggraaql--klsscpsgrq 273
QY 60 -PLLLDARTLDPQGAPPAGWEVDFVWQGLRH-OPWKQLCLELRAAWGELDAGEAEARAG 117
DB 274 PASLIDVRSV--pgldsgwvfdiwlfrnknsaqiclele-aw---ergra----- 321
QY 118 PQOPPPDLRLSGFGRVRRPQERALLVVFTRSORKNL-FAEMREQLGSAEAGPGAGAE 176
DB 322 -----vdlrglfgdraarqvhekalfivgrtkrdlffneikarsgddkt----- 368
QY 177 GSWPPPGAPDARPLSPGRRRTAFASRHGKRHKSKRLRCSKKPLHVNFKELGWDD 236
DB 369 -----vyeylfsq-rrkrraplratqgkrpsknkarscrkalhvnfdmgwdd 416
QY 237 WIAPLEYAYHCEGVGDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPISI 296
DB 417 WIAPLEYAEAFHCEGLCEFLPRLSHLEPTNHAVIQLMNSMDPESTPPTCCVPTRLSPISI 476
QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
DB 477 lfidsannvvykyedmvvescgr 501

RESULT 11
AAW36100
ID AAW36100 standard; Protein: 501 AA.
```


Db 274 paslldvrsv--pgldsgwevdiwklfrnknsaqclclele-aw---ergra----- 321
 QY 118 POQPPPDLSLGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 176
 Db 322 -----vdrlgldfdaarqvhkalfvgrtkkrdlffneikarsgqddkt----- 368
 QY 177 GSWPPPGAPDARPLPSPGRRRRRTAFASRHGKSRKSLRCLPLHVNFKELGWDD 236
 Db 369 -----vyeylfsq-rrkraplratqgkrpsknlkarsckalhnvfkmgwdd 416
 QY 237 WIIAPLEYAYHCEGVCDPPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 296
 Db 417 wiiapleyeafhceglcelflrshleptnhaviqtlmsmdpestptccvptrlspisi 476
 QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
 Db 477 lfidsannvvykyedmvvescgr 501

RESULT 15

AAW12770
 AAW12770 standard; Protein; 501 AA.
 AAW12770:
 11-MAY-1997 (first entry)
 Human bone morphogenic factor MP52 Arg.
 Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
 connective tissue; mucous membrane; epithelium; teeth;
 wound healing; vulnary; tissue regeneration; osteoporosis;
 bone fracture; dental implant; osteoblast.
 Homo sapiens.
 Key Location/Qualifiers
 Peptide 1..27
 /label= Sig_peptide
 Cleavage-site 380..381
 /note= "sequencing suggests MP52 Arg is processed
 proteolytically at Arg380-Arg381"
 Cleavage-site 381..382
 /note= "alternative cleavage site at Arg381-Ala382"
 Mat_protein 381..501
 /label= Mat_protein
 /note= "mature MP52 Arg preferred for use in
 compsns. of the invention"

WO9706254-A1.
 20-FEB-1997.
 02-AUG-1996; 96WO-EP03427.
 03-AUG-1995; 95EP-0112241.
 (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
 Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
 WPI: 1997-154261/14.
 N-PSDB; AAT59729.

New human bone morphogenic factor, MP52 Arg - used in the treatment
 of osteoporosis and bone fracture, and for promoting bone regrowth
 Claim 1; Page 12-15; 26pp; English.
 Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
 factor that induces formation of cartilage from undifferentiated
 mesenchymal cells and which stimulates the differentiation and
 maturation of osteoblasts. It is effective for treating/preventing

CC bone diseases caused by abnormal bone metabolism such as
 CC osteoporosis. It also accelerates the healing of bone fractures,
 CC and is useful for orthopaedic reconstruction, bone transplantation,
 CC and dental therapeutics because of its bone morphogenetic activity.
 CC It is also effective for preventing/treating cartilage, skin,
 CC connective tissue, mucous membrane, teeth and epithelial disorders.
 CC Recombinant MP52 Arg can be produced in host (e.g. CHO) cells
 CC utilising an isolated DNA sequence (AAT59729) in plasmid pMS599.
 XX
 SQ Sequence 501 AA;
 Query Match 43.9%; Score 771; DB 18; Length 501;
 Best Local Similarity 51.1%; Pred. No. 1.7e-60;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;
 QY 9 LRRQKLYFDVSMLSKDELVEALRLFRQAPS-----APWPPAGPLRHVQLFPCLSL--- 59
 Db 217 vrkqrvfdisal-ekdgilgaelrilkkpsdtakpaapgggraql--klsscpgrq 273
 QY 60 -PLLLDARTLDPOGAPPAGWEVDFVWQGLRH-OPWKQLCLELRANGELDAGEAEARARG 117
 Db 274 paslldvrsv--pgldsgwevdiwklfrnknsaqclclele-aw---ergra----- 321
 QY 118 POQPPPDLSLGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 176
 Db 322 -----vdrlgldfdaarqvhkalfvgrtkkrdlffneikarsgqddkt----- 368
 QY 177 GSWPPPGAPDARPLPSPGRRRRRTAFASRHGKSRKSLRCLPLHVNFKELGWDD 236
 Db 369 -----vyeylfsq-rrkraplratqgkrpsknlkarsckalhnvfkmgwdd 416
 QY 237 WIIAPLEYAYHCEGVCDPPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 296
 Db 417 wiiapleyeafhceglcelflrshleptnhaviqtlmsmdpestptccvptrlspisi 476
 QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
 Db 477 lfidsannvvykyedmvvescgr 501

Search completed: October 3, 2002, 15:38:39
 Job time: 320 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 15:39:08 ; Search time 23.43 seconds
(without alignments)
334.640 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDSLHTPLRRQKYLFDVSM.....GNVYKQYEDMVESGCGR 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

al number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1757	100.0	321	1	US-08-362-670B-26
2	1757	100.0	321	3	US-08-333-576C-26
3	1757	100.0	321	4	US-08-808-324-26
4	1757	100.0	321	5	PCT-US94-14030A-26
5	1202.5	68.4	263	1	US-08-362-670B-32
6	1202.5	68.4	263	3	US-08-333-576C-32
7	1202.5	68.4	263	4	US-08-808-324-32
8	1202.5	68.4	263	5	PCT-US94-14030A-32
9	771	43.9	401	3	US-08-289-222E-3
10	771	43.9	401	4	US-09-054-526B-3
11	771	43.9	501	2	US-08-288-508C-2
12	765	43.5	388	1	US-08-362-670B-34
13	765	43.5	388	3	US-08-333-576C-34
14	765	43.5	388	4	US-08-808-324-34
15	765	43.5	388	5	PCT-US94-14030A-34
16	765	43.5	495	1	US-08-455-559-10
17	765	43.5	495	4	US-09-145-060-10
18	765	43.5	495	5	PCT-US94-00857-10
19	731	41.6	134	1	US-08-581-529B-6
20	731	41.6	134	3	US-09-097-616-6
21	731	41.6	134	5	PCT-US94-07762-6
22	691.5	39.4	294	1	US-08-362-670B-2
23	691.5	39.4	294	3	US-08-333-576C-2
24	691.5	39.4	294	4	US-08-808-324-2
25	691.5	39.4	294	5	PCT-US94-14030A-2
26	661	37.6	119	1	US-08-581-529B-7
27	661	37.6	119	3	US-09-097-616-7

28	661	37.6	119	5	PCT-US94-07762-7	Sequence 7, Appl
29	618	35.2	240	1	US-08-362-670B-30	Sequence 30, Appl
30	618	35.2	240	3	US-08-333-576C-30	Sequence 30, Appl
31	618	35.2	240	4	US-08-808-324-30	Sequence 30, Appl
32	618	35.2	240	5	PCT-US94-14030A-30	Sequence 30, Appl
33	584	33.2	411	1	US-08-362-670B-28	Sequence 28, Appl
34	584	33.2	411	3	US-08-333-576C-28	Sequence 28, Appl
35	584	33.2	411	4	US-08-808-324-28	Sequence 28, Appl
36	584	33.2	411	5	PCT-US94-14030A-28	Sequence 28, Appl
37	553	31.5	161	2	US-08-581-528A-6	Sequence 6, Appl
38	553	31.5	161	5	PCT-US94-07799-6	Sequence 6, Appl
39	549	31.2	119	1	US-08-455-559-13	Sequence 13, Appl
40	549	31.2	119	4	US-09-145-060-13	Sequence 13, Appl
41	549	31.2	119	5	PCT-US94-00657-13	Sequence 13, Appl
42	549	31.2	120	1	US-08-362-670B-4	Sequence 4, Appl
43	549	31.2	120	3	US-08-333-576C-4	Sequence 4, Appl
44	549	31.2	120	4	US-08-808-324-4	Sequence 4, Appl
45	549	31.2	120	5	PCT-US94-14030A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-362-670B-26
: Sequence 26, Application US/08362670B
: Patent No. 5658882
: GENERAL INFORMATION:
: APPLICANT: Celeste, Anthony J.
: APPLICANT: Wozney, John
: APPLICANT: Rosen, Vicki A.
: APPLICANT: Wolfman, Neil
: APPLICANT: Thomsen, Gerald H.
: APPLICANT: Melton, Douglas A.
: TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENETICS INSTITUTE, INC.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,670B
: FILING DATE: December 22, 1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Lazar, Steven R.
: REGISTRATION NUMBER: 32,618
: REFERENCE/DOCKET NUMBER: 5202-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617 498-8260
: TELEFAX: 617 876-5851
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 321 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-362-670B-26

Query Match 100.0% Score 1757; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-147;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NSDSLHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLPCLSP 60

Db 1 NSDLSTPLRQKYLFDVSMLEKEELVGAELRLFRQAPSAPWGPAGPLHVQLFPCCLSP 60
QY 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPKWQKQCLLELRAAAGELDAGEAARAGPQQ 120
Db 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPKWQKQCLLELRAAAGELDAGEAARAGPQQ 120
QY 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
Db 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
QY 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
Db 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
QY 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
Db 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
Db 301 AGNNVYKQYEDMVVESCGR 321

RESULT 2

US-08-333-576C-26
; Sequence 26, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333.576C
; FILING DATE: No. 6027919ember 2, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-576C-26

Query Match 100.0%; Score 1757; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-147;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSDLSTPLRQKYLFDVSMLEKEELVGAELRLFRQAPSAPWGPAGPLHVQLFPCCLSP 60
Db 1 NSDLSTPLRQKYLFDVSMLEKEELVGAELRLFRQAPSAPWGPAGPLHVQLFPCCLSP 60
QY 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPKWQKQCLLELRAAAGELDAGEAARAGPQQ 120
Db 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPKWQKQCLLELRAAAGELDAGEAARAGPQQ 120
QY 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
Db 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
QY 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
Db 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
QY 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
Db 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
Db 301 AGNNVYKQYEDMVVESCGR 321

RESULT 3

US-08-808-324-26
; Sequence 26, Application US/08808324
; Patent No. 6284872
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,324
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-808-324-26

Query Match 100.0%; Score 1757; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-147;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLPCLSP 60
DB 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLPCLSP 60
QY 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHQPWKQLCLLELRAAWGELDAGEAARAGPQO 120
DB 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHQPWKQLCLLELRAAWGELDAGEAARAGPQO 120
QY 121 PPPDLRLSGFGRVRRPQERALLVFTRSQKKNLFAEMREQLGSAAAGPGAGAGSWP 180
DB 121 PPPDLRLSGFGRVRRPQERALLVFTRSQKKNLFAEMREQLGSAAAGPGAGAGSWP 180
QY 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELGWDWIIA 240
DB 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELGWDWIIA 240
QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
DB 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
DB 301 AGNNVYKQYEDMVVESCGR 321

RESULT 4
PCT-US94-14030A-26
; Sequence 26, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Bridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14030A
; FILING DATE: Berewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,103
; FILING DATE: 07-DEC-1993
; APPLICATION NUMBER: US 08/217,780
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 08/333,576
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202D-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14030A-26

Query Match 100.0%; Score 1757; DB 5; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-147;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLPCLSP 60
DB 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLPCLSP 60
QY 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHQPWKQLCLLELRAAWGELDAGEAARAGPQO 120
DB 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHQPWKQLCLLELRAAWGELDAGEAARAGPQO 120
QY 121 PPPDLRLSGFGRVRRPQERALLVFTRSQKKNLFAEMREQLGSAAAGPGAGAGSWP 180
DB 121 PPPDLRLSGFGRVRRPQERALLVFTRSQKKNLFAEMREQLGSAAAGPGAGAGSWP 180
QY 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELGWDWIIA 240
DB 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELGWDWIIA 240
QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
DB 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
DB 301 AGNNVYKQYEDMVVESCGR 321

RESULT 5
US-08-362-670B-32
; Sequence 32, Application US/08362670B
; Patent No. 5658882
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Bridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,670B
; FILING DATE: December 22, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-670B-32

Query Match 68.4%; Score 1202.5; DB 1; Length 263;
Best Local Similarity 83.3%; Pred. No. 9.3e-99;
Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;
QY 46 PAGPLHVQLFPCLSPLLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKQLCLELRAANGE 105
DB 7 PAG-----PTLRGSSGTQPR---PAG-KSFDVWQGLRPPQWKQLCLELRAANGE 51
QY 106 LDAGEAEARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREOLGS 165
DB 52 LDAGDGTGARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREOLGS 111
QY 166 AEAAGPAGAGSGSWPPSGAPDARPLSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 225
DB 112 AEA---AGAGSCPAPSGSDTGSWLPSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 167
QY 226 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 285
DB 168 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 227
QY 286 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 321
DB 228 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 263

RESULT 6
US-08-333-576C-32
; Sequence 32, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,576C
; FILING DATE: No. 6027919ember 2, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-576C-32

Query Match 68.4%; Score 1202.5; DB 3; Length 263;
Best Local Similarity 83.3%; Pred. No. 9.3e-99;

Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;
QY 46 PAGPLHVQLFPCLSPLLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKQLCLELRAANGE 105
DB 7 PAG-----PTLRGSSGTQPR---PAG-KSFDVWQGLRPPQWKQLCLELRAANGE 51
QY 106 LDAGEAEARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREOLGS 165
DB 52 LDAGDGTGARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREOLGS 111
QY 166 AEAAGPAGAGSGSWPPSGAPDARPLSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 225
DB 112 AEA---AGAGSCPAPSGSDTGSWLPSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 167
QY 226 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 285
DB 168 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 227
QY 286 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 321
DB 228 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 263

RESULT 7
US-08-808-324-32
; Sequence 32, Application US/08808324
; Patent No. 6284872
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,324
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-808-324-32

Query Match 68.4%; Score 1202.5; DB 4; Length 263;
Best Local Similarity 83.3%; Pred. No. 9.3e-99;
Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLSPLLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKQLCLELRAANGE 105

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Db      7  PAG-----PTLRGSSGTQPR---PAG-KSFDVWQGLRPPQWKQLCLELRANGE 51
QY     106 LDAGEAEARARGPQQPPDLRLSLGFGRRVRPPQERALLVVFTRSORKNLFAEMREOLGS 165
Db      52 LDXGDTGARARGPQQPPDLRLSLGFGRRVRPPQERALLVVFTRSORKNLFTHEHEOLGS 111
QY     166 AEAAGPAGAGSGSWPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHKKSRLRCSKKPL 225
Db     112 AEA-----AGAGSCPARSGSDTGSWLPSPGRRRRRTAFASRHGKRHKKSRLRCSKKPL 167
QY     226 HVNFKEGLGDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIOTLMSMDPGSTPPSC 285
Db     168 HVNFKEGLGDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIOTLMSMDPGSTPPSC 227
QY     286 CVPTKLTPISTILYIDAGNNVYKQYEDMVVESCGR 321
Db     228 CVPTKLTPISTILYIDAGNNVYKQYEDMVVESCGR 263

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ULT 8

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; Sequence 32, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US94/14030A
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,103
; FILING DATE: 07-DEC-1993
; APPLICATION NUMBER: US 08/217,780
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 08/333,576
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202D-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-14030A-32

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Query Match      68.4%; Score 1202.5; DB 5; Length 263;
Best Local Similarity 83.3%; Pred. No. 9.3e-99;
Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;
QY     46 PAGPLHVQLFPCLSPDLLDARTLDQAGPPAGWVEFDVWQGLRPPQWKQLCLELRANGE 105

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Db      7  PAG-----PTLRGSSGTQPR---PAG-KSFDVWQGLRPPQWKQLCLELRANGE 51
QY     106 LDAGEAEARARGPQQPPDLRLSLGFGRRVRPPQERALLVVFTRSORKNLFAEMREOLGS 165
Db      52 LDXGDTGARARGPQQPPDLRLSLGFGRRVRPPQERALLVVFTRSORKNLFTHEHEOLGS 111
QY     166 AEAAGPAGAGSGSWPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHKKSRLRCSKKPL 225
Db     112 AEA-----AGAGSCPARSGSDTGSWLPSPGRRRRRTAFASRHGKRHKKSRLRCSKKPL 167
QY     226 HVNFKEGLGDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIOTLMSMDPGSTPPSC 285
Db     168 HVNFKEGLGDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIOTLMSMDPGSTPPSC 227
QY     286 CVPTKLTPISTILYIDAGNNVYKQYEDMVVESCGR 321
Db     228 CVPTKLTPISTILYIDAGNNVYKQYEDMVVESCGR 263

RESULT 9
US-08-289-222E-3
; Sequence 3, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; TITLE OF INVENTION: FAMILY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARCELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; CITY: SUITE 330
; STATE: WASHINGTON
; COUNTRY: DC
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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RESULT 15
PCT-US94-14030A-34
; Sequence 34, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
[CT-US94-14030A-34

Query Match 43.5%; Score 765; DB 5; Length 388;
Best Local Similarity 51.2%; Pred. No. 6.3e-60;
Matches 172; Conservative 36; Mismatches 78; Indels 50; Gaps 10;

QY 12 QYLFVMSLSEKELVGAELRFRQ-APSAPWGPAGPLHVQLFPC-----LSPLLLDAR 66
DB 77 QSFLEFVSSLNDADVGAELRVLRRGSPESGPGSWTSPPLLLLLSTCPGAARAPRLLYSR 136

QY 67 TLDPQCAPPGAGVEFVWQGLRH-----OPWKQLCLELRAAWGELDAGEAEARARGPOOP 121
DB 137 AAEP--LVQORWEAFDADAMRRHRRPRPPRAFCLLLRAVAGPV-----P 180

QY 122 PPDLRLSGF---GRRVRPPQERALLVYVTRSQRK-NLFAEMREQ---LGSAAEAGPGAG 174
DB 181 SPLALRLGFGWPGGGSAAEERAVLVVSSRTQRKESLFEIRAQARALGAALASEP--- 237

QY 175 AEGSWPPPGAPDAPRWLPSPGRRRRRTAFASRH-----GKRHCKKSRLRCSKKPL 225
DB 238 -----LPDPGTGTASPRAVIGRRRRRTALAGTRTAQGGGGAGRGHGRGRSRSRKPL 292

QY 226 HYNFKELGWDHIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPPSC 285
DB 293 HVDFKELGWDHIIAPLEYAYHCEGLCDFPLRSHLEPTNHAIIQTLNMAPDAAPASC 352

QY 286 CVPTKLPTISILYIDAGNNVYKQYEDMVVESCGR 321
DB 353 CVPARLSPISILYIDANNVYKQYEDMVVEACGR 388

Search completed: October 3, 2002, 15:39:09
Job time: 235 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 15:39:44 ; Search time 29.81 Seconds
(without alignments)
1034.709 Million cell updates/sec

Title: US-09-945-182-26
Perfect score: 1757
Sequence: 1 NSDLSHTPLRRQKYLFDVSM.....GNVVYKQYEDMVVESCGR 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1368	77.9	436	2 B55452	cartilage-derived
2	771	43.9	501	2 JC2347	growth/differentia
3	765	43.5	495	2 S43294	bone morphogenetic
4	762	43.4	501	2 A55452	cartilage-derived
5	691	39.3	125	2 S43295	bone morphogenetic
6	549	31.3	151	2 S43296	bone morphogenetic
7	426.5	24.3	398	2 JH0588	bone morphogenetic
8	425.5	24.2	398	2 JH0587	bone morphogenetic
9	418.5	23.8	405	2 I50608	bone morphogenetic
10	406.5	23.1	408	1 BMH04	bone morphogenetic
11	405.5	23.1	452	2 I49542	bone morphogenetic
12	405.5	23.1	461	2 S52408	SPDVR1 protein - s
13	401	22.8	393	2 S37073	bone morphogenetic
14	401	22.8	420	2 I49541	bone morphogenetic
15	396.5	22.6	454	1 BMH05	bone morphogenetic
16	396	22.5	408	2 S38343	bone morphogenetic
17	395	22.5	394	2 S45355	bone morphogenetic
18	391	22.3	408	2 JH0801	bone morphogenetic
19	388.5	22.1	396	1 BMH02	bone morphogenetic
20	387	22.0	430	2 JQ1184	osteogenic protein
21	386	22.0	431	1 BMH07	bone morphogenetic
22	385.5	21.9	402	2 A45056	osteogenic protein
23	384	21.9	313	2 I51284	bone morphogenetic
24	384	21.9	426	2 JH0690	bone morphogenetic
25	379	21.6	400	2 A49147	bone morphogenetic
26	378	21.5	408	2 S58791	bone morphogenetic
27	377	21.5	401	2 JH0689	bone morphogenetic
28	375	21.3	353	2 I50607	bone morphogenetic
29	369	21.0	588	2 A26158	decapentaplegic pr

30 362.5 20.6 354 2 S29718 gene nodal protein
31 360 20.5 510 2 A54798 Vg-1-related prote
32 351 20.0 513 1 BMH06 bone morphogenetic
33 343 19.5 365 2 T43286 cat-1 protein - Ca
34 339.5 19.3 427 2 A40735 TGF beta homolog d
35 334 19.0 207 2 S37618 vgr protein - rat
36 332 18.9 455 2 A43918 TGF-beta-related p
37 328 18.7 478 2 JC4838 bone morphogenetic
38 324.5 18.5 360 2 A29619 Vgi embryonic grow
39 312 17.8 476 2 JC4646 bone morphogenetic
40 308 17.5 372 2 C39364 GDF-1 embryonic gr
41 299 17.0 366 2 A46607 growth/differentia
42 293 16.7 472 1 BMH03 bone morphogenetic
43 292.5 16.6 426 1 B24248 inhibit beta-A cha
44 290 16.5 366 2 A54502 transforming growt
45 289.5 16.5 424 1 WFPGBA inhibit beta-A cha

ALIGNMENTS

RESULT 1

B55452
cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
C:Accession: B55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K.
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming g:
A:Reference number: A55452; MUID:95050604
A:Accession: B55452
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-436 <CHA>
A:Cross-references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490
C:Superfamily: inhibit

Query Match 77.9%; Score 1368; DB 2; Length 436;
Best Local Similarity 81.7%; Pred. No. 2e-95;
Matches 268; Conservative 9; Mismatches 39; Indels 12; Gaps 6;

QY 3 DLSHTPLRRQKYLFDVSMISDKELVGAELRFRQAPSAPWGPAGPLHVQLFPCLSPLL 62
DB 112 DLSHTPLRRQKYLFDVSTLSKDELVGADVRLFRQAPALAPPAAALRALP-VAPAA 170
QY 63 LDARTLDPOGAPPAGWEVDVWGQHRQKQLCLRLAAW-CELDAGAEARARGPOOP 121
DB 171 GSAEP-GPACAPRPGWEVDVWRGLRQPQWKQLCLRLAAWGEPCAAEDEARTPGPOOP 229
QY 122 PPDLSLGLGRRVRPQERALLVFTSRQKNLFAEMRQLGSA-EAAGPGAGAGSGW- 179
DB 230 PPDLSLGLGRRVRPQERALLVFTSRQKNLFAEMRQLGSA-EAAGPGAGAGSGW- 289
QY 180 -----PPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHKSRKSLRCSKKPLHVNFKELG 233
DB 290 PPPPPPPPSGTPDAGLWSPSG-RRRTAFASRHGKRHKSRKSLRCSKKPLHVNFKELG 348
QY 234 WDDWIIAPLEYAYHCEGVCDFFLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTP 293
DB 349 WDDWIIAPLEYAYHCEGVCDFFLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTP 408
QY 294 ISILYIDAGNNVYKQYEDMVVESCGR 321
DB 409 ISILYIDAGNNVYKQYEDMVVESCGR 436

RESULT 2

JC2347
growth/differentiation factor 5 - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000

C:Accession: JC2347
R:Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A:Title: Cloning and expression of recombinant human growth/differentiation factor 5.
A:Reference number: JC2347; MUID:95071375
A:Accession: JC2347
A:Molecule type: DNA
A:Residues: 1-501 <HO>
A:Cross-references: GB:X80915; MID:g671524; PIDN:CAA56874.1; PID:g671525
C:Genetics:
A:Gene: GDB:BMP9
A:Cross-references: GDB:433948
A:Introns: 211/1
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:189/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKYLFDVSMDSKELVGAELRLFRQAPS-----APWGPPAGPLHVQLFPCLSL--- 59
Db 217 VRKQRYVFDISAL-EKDGLLGAELRLRKPSDTAKPAAPGGGAAQL--KLSSCPSGRQ 273

Qy 60 -PLLDARTLDPQAGPAGWEVDVWQGLRH-OPWKQLCLLELAANGELDAGEAEARAG 117
Db 274 PASLLDVRSV--PGLDGSWEVDFINKLFRNFKNSAQLCLELE-AW---ERGRA----- 321

Qy 118 POQPPPPDLRLSGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAAAGPGAGAE 176
Db 322 -----VDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKT----- 368

Qy 177 GSWPPSGAPDARWLPSPGRRRRRTAFASRHGKSRKLRCSKPLHVNFKELGWDW 236
Db 369 -----VVEYLFQ--RRKRRAPLATRQGRKPSKRLKARCSRKALHVNFKDGMGDD 416

Qy 237 WIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 296
Db 417 WIIAPLEYEAFHCEGLCEFPRLSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPIS 476

Qy 297 LYIDAGNNVYKQYEDMVVESCGR 321
Db 477 LFIDSANNVYKQYEDMVVESCGR 501

RESULT 3
43294
One morphogenetic protein-related protein (GDF5) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C:Accession: S43294
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427
A:Accession: S43294
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <STO>
A:Cross-references: GB:008337; NID:g488461; PIDN:AAA18778.1; PID:g488462
C:Superfamily: inhibin

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Qy 9 LRRQKYLFDVSMDSKELVGAELRLFRQAP---SAPWGPPAGPL-HVQLFPCLSL---P 60
Db 211 VRKQRYVFDISAL-EKDGLLGAELRLRKPLDVAPSPSGRVAQLKLSSCPSGRQPA 269

Qy 61 LLLDARTLDPQAGPAGWEVDVWQGLRH-OPWKQLCLLELAANGELDAGEAEARAGPQ 119
Db 270 ALLDVRSV--PGLDGSWEVDFINKLFRNFKNSAQLCLELE-AW---ERGRA----- 315

Qy 120 QPPPPDLRLSGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAAAGPGAGAGS 178
Db 316 ---VDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKT----- 362

Qy 179 WPPSGAPDARWLPSPGRRRRRTAFASRHGKSRKLRCSKPLHVNFKELGWDW 238
Db 363 -----VVEYLFQ--RRKRRAPLATRQGRKPSKRLKARCSRKALHVNFKDGMGDDW 412

Qy 239 IAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 298
Db 413 IAPLEYEAFHCEGLCEFPRLSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPIS 472

Qy 299 IDAGNNVYKQYEDMVVESCGR 321
Db 473 IDSANNVYKQYEDMVVESCGR 495

RESULT 4
A55452
cartilage-derived morphogenetic protein 1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
C:Accession: A55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; J.
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming
A:Reference number: A55452; MUID:95050604
A:Accession: A55452
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-501 <CHA>
A:Cross-references: GB:U13660; NID:g600731; PID:g600732
C:Genetics:
A:Gene: GDB:CDMP1
A:Cross-references: GDB:438940
C:Superfamily: inhibin

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Qy 9 LRRQKYLFDVSMDSKELVGAELRLFRQAPSAPWGPPAGP-----LHVQLFPCLSL--- 59
Db 217 VRKQRYVFDISAL-EKDGLLGAELRLRKPS-DTAKPAVPRSRRAAQLKLSSCPSGRQ 274

Qy 60 PLLDARTLDPQAGPAGWEVDVWQGLRH-OPWKQLCLLELAANGELDAGEAEARAGP 118
Db 275 ALLDVRSV--PGLDGSWEVDFINKLFRNFKNSAQLCLELE-----EAWERGR-- 320

Qy 119 QPPPPDLRLSGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAAAGPGAGAG 177
Db 321 ---TVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKT----- 368

Qy 178 SWPPSGAPDARWLPSPGRRRRRTAFASRHGKSRKLRCSKPLHVNFKELGWDW 237
Db 369 -----VVEYLFQ--RRKRRAPLATRQGRKPSKRLKARCSRKALHVNFKDGMGDDW 417

Qy 238 IAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 297
Db 418 IAPLEYEAFHCEGLCEFPRLSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPIS 477

Qy 298 YIDAGNNVYKQYEDMVVESCGR 321
Db 478 FIDSANNVYKQYEDMVVESCGR 501

RESULT 5

S43295

bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
M:Alternate names: growth and differentiation factor 6
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C:Accession: S43295
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the F:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
A:Reference number: S43294; MUID:94195427
A:Accession: S43295
A:Molecule type: DNA
A:Residues: 1-125 <STO>
A:Cross-references: EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g488464
C:Genetics:
A:Gene: gdf6
C:Superfamily: inhibin
F:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
F:6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <M

Query Match 39.3%; Score 691; DB 2; Length 125;
Best Local Similarity 99.2%; Pred. No. 4.1e-45;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 197 RRRRTAPASRHGKRRGKSKRLRCKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDP 256
Db 1 RRRRTAPASRHGKRRGKSKRLRCKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDP 60
QY 257 LRSLEPTAHIIQTLLNSMDPGSTPPSCCVPTKLPISILYIDAGNNVVYKQYEDMVVE 316
Db 61 LRSLEPTAHIIQTLLNSMDPGSTPPSCCVPTKLPISILYIDAGNNVVYKQYEDMVVE 120
QY 317 SCGR 321
Db 121 SCGR 125

RESULT 6

S43296
bone morphogenetic protein-related protein (GDF7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C:Accession: S43296
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the F:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
A:Reference number: S43294; MUID:94195427
A:Accession: S43296
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g488466
C:Superfamily: inhibin

Query Match 31.2%; Score 549; DB 2; Length 151;
Best Local Similarity 59.5%; Pred. No. 2.3e-34;
Matches 103; Conservative 13; Mismatches 35; Indels 22; Gaps 1;
QY 149 RSQRKNLFAHREOLGSAEAGPGAGAGSWPPPGAPDARPLWPSGRRRRRTAFASRH 208
Db 1 RRRRTALACTGAQGGGGGGGGGGGGGGGGA----- 38
QY 209 GRRGKSKRLRCKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDPPLRSHLEPTNHAI 268
Db 39 GRGHRGRRGKSKRLSHVDFKELGWDWIIAPLDYAYHCEGVCDPPLRSHLEPTNHAI 98
QY 269 IOTLLNSMDPGSTPPSCCVPTKLPISILYIDAGNNVVYKQYEDMVVEGCGR 321
Db 99 IOTLLNSMDPGSTPPSCCVPARLSPISILYIDAGNNVVYKQYEDMVVEACGCR 151

RESULT 7

JH0688
bone morphogenetic protein 2II precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0688
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in ear:
A:Reference number: JH0687; MUID:92378616
A:Accession: JH0688
A:Molecule type: mRNA
A:Residues: 1-398 <NIS>
A:Cross-references: GB:X63425; NID:g64583; PIDN:CAA45019.1; PID:g64584
A:Experimental source: oocyte
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
F:137,202,237,340/Binding site: carbonyl site: Asn (covalent) #status predicted

Query Match 24.3%; Score 426.5; DB 2; Length 398;
Best Local Similarity 31.3%; Pred. No. 9.7e-25;
Matches 104; Conservative 51; Mismatches 90; Indels 87; Gaps 12;
QY 12 QKYLFDVSMLSKDELVGAEELRFRQAPSAPWGPAGPLH-VOLPCLSLP----- 61
Db 132 QRFFNLSSIPDEELVTSELRIREFQVOEPKTCGSKLHRINIYDIYKPAAMASRGPVV 191
QY 62 -LLDARTLDPOCAPAGWVDFVWQGL-----RHQPWKOLCLLELAANGELDAGAEARA 115
Db 192 RLDDTLRIHN--ESKWESEFDTPTAIRWIAHKQPNHGFEVVEVTHLNDNTNPKRHVRI 248
QY 116 RGPQPPPPDLRLS-----GFGRRVRPPQRRALLYVFTSRQKNLFAEMREQLSAEAGP 171
Db 249 S-----RSLTDKGHWPRIRP-----LLVTFSHD-----GK 274
QY 172 GAGAECSPPPGAPDARPLWPSGRRRRRTAFASRRGKRRGKSKRLR--CSKKPLHVN 229
Db 275 GHALH-----KQKQQA-----RHQKRLKSSCRRHPLYVDF 307
QY 230 KELGWDWIIAPLEYAYHCEGVCDPPLRSHLEPTNHAIOTLLNSMDPGSTPPSCCVPT 289
Db 308 SDVGWMDWIVAPPGYHAFYCHGCEPPLADHLNSTHAIQVTLVNSVT-NIPKACCVPT 366
QY 290 KLTPISILYIDAGNNVVYKQYEDMVVEGCGR 321
Db 367 ELASISMLYLDENKXVYKQYEDMVVEGCGR 398

RESULT 8

JH0687
bone morphogenetic protein 2I precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0687; S16244
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in ear:
A:Reference number: JH0687; MUID:92378616
A:Accession: JH0687
A:Molecule type: mRNA
A:Residues: 1-398 <NIS>
A:Cross-references: GB:X63424; NID:g64585; PIDN:CAA45018.1; PID:g64586
A:Experimental source: oocyte
R:Plessow, S.; Koester, M.; Knoechel, W.
Biochim. Biophys. Acta 1089, 280-282, 1991
A:Title: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
A:Reference number: S16244; MUID:91274367
A:Accession: S16244
A:Molecule type: mRNA
A:Residues: 1-6,'S',8-15,'V',17-232,'N',234-398 <PLE>
A:Cross-references: EMBL:X55031; NID:g64581; PIDN:CAA38850.1; PID:g64582

R:King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.

Dev. Biol. 166, 112-122, 1994

A:Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice

A:Reference number: 149542; MUID:95046894

A:Accession: 149542

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-452 <RES>

A:Cross-references: GB:L41145; NID:g755033; PIDN:AAA64612.1; PID:g755034

C:Genetics:

A:Gene: BMP5

C:Superfamily: inhibin

Query Match 23.1%; Score 405.5; DB 2; Length 452;

Best Local Similarity 29.0%; Pred. No. 4.2e-23;

Matches 96; Conservative 54; Mismatches 126; Indels 55; Gaps 8;

QY 1 NSDLSHTPLRRKQYLFVDSVMSLSDKEELVCAELRFRQAPSAPWGPAGPLHWLFPCLSP 60

165 DKDFSHQRHYKEFREDLTOIPHGCAVAAAEFRYKDKGNIRFENET--IKISYQIIE 222

QY 61 -----LLDARTLDPOGAPPAGWCFVDMQGLRH---QFWKOLCCLLELAAMGELDAG 109

223 YTNRADLFLDTRKTQ---ALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGD---G 276

QY 110 EAEARAGPQQPPDLRLSLGRRVRPQERALLVYTRSQKMLFAEMREQLGSABAA 169

DL 277 RS-----INVKSAGLVGRHQPSQKPPFMAFFKASE-----VLLRSVRAASRRK 320

QY 170 GPCGAGEGSWPPSGAPDARPLSPGRRRRRTAFASRHGKRHGKSLRCSKKPLHWNF 229

Db 321 NQNRKNSHQDPSPMPA-----GDYNTSEQKQACKKHLYVSF 360

QY 230 KELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCVPT 289

Db 361 RDLGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCVPT 420

QY 290 KLTPISILYIDAGNNVYKQYEDMVVESC GC 320

Db 421 KLNALSVLYFDSSNVILKKYRNMVVRSCGC 451

RESULT 12

S52408

SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999

Accession: S52408

Submitted to the EMBL Data Library, February 1995

A:Reference number: S52408

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <PONS>

A:Cross-references: EMBL:Z48313; NID:9673496; PID:9673497

C:Superfamily: inhibin

Query Match 23.1%; Score 405.5; DB 2; Length 461;

Best Local Similarity 32.4%; Pred. No. 4.2e-23;

Matches 108; Conservative 42; Mismatches 104; Indels 79; Gaps 12;

QY 13 KYLFDVMSLSDKEELVCAELRFRQAPSAPWGPAGPLHWLFPCLSP 66

Db 182 RYRFDIGRIPOGETVTSALRVRDRA--GRQGRSLYRIDVLLRRSGDSRSPYLDST 239

QY 67 TLDPOGAPPAGWCFVDMQGLRH---QFWKOLCCLLELAAMGELDAGAPARAGPQQ 120

Db 240 IV---CAGDHWLVDMVTSATSTW---RSYPCANVGLQLRVE--SLQGLNID----- 283

QY 121 PPPDLRLSLGRRVRPQERALLVYTRSQ-----RKNLFAEMREQLGSAAAGP 171

Db 284 --PTDAGVVGNGN--NEGREFPMVFFORNEEVATSHLRRNRRAATROKKG----- 332

QY 172 GAGAGSWPPSGAPDARPLSPGRRRR---TAFASRHGKRHGKSLRCSKKPLHV 227

Db 333 -----GKRPRKPDNDIASR--DSASSLNSDWQCKRKNLFV 367

QY 228 NFKELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCV 287

Db 368 NFKELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCV 427

QY 288 PTCLTPISILYIDAGNNVYKQYEDMVVESC GC 320

Db 428 PTKLSPITVLVYDSSNRNVLLAKYRNMVVRACGC 460

RESULT 13

S37073

bone morphogenetic protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)

Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999

Accession: S37073

R:Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.

submitted to the EMBL Data Library, September 1993

A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic pro

A:Reference number: S37073

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-393 <PENS>

A:Cross-references: EMBL:Z25868; NID:g397950; PIDN:CAA81088.1; PID:g397951

C:Superfamily: inhibin

Query Match 22.8%; Score 401; DB 2; Length 393;

Best Local Similarity 30.8%; Pred. No. 7.9e-23;

Matches 105; Conservative 50; Mismatches 98; Indels 88; Gaps 13;

QY 2 SDSLHTPLRRKQYLFVDSVMSLSDKEELVCAELRFRQAPSAPWGPAGPLHWLFPCLSP 61

Db 120 SEMSGKTSRR--FFENLSSVPTDEFLTSAELQIFREOMQALGNSFQHRINIYEIKPA 177

QY 62 -----LLDARTLDPOGAPPAGWCFVDMQGLRHOPWKQLCCLLELAAMGELDAGEA 111

Db 178 TASSKFPVTRLDTRLVTON---TSQWESFDVTPAVMR--W-----TAQHTNHGFV 224

QY 112 EARGPQQPPPPDLRLSLGRRVRPQERALLVYTRSQKMLFAEMREQLGSAAAGP 171

Db 225 VEVAHLEKP-----GVSKR-----HVRISRLHOD----- 250

QY 172 GAGAGSWPPSGAPDARPLSPG-----RRRRTAFASRHGKRHGKSLR--C 220

Db 251 ----EHSW-----SQVRPLLVTFEGHCKGHPKREKQA-----KKQRKRLKSSC 293

QY 221 SKKPLHVNFKELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDP 280

Db 294 KRHLVYDFSDVGNWDMIVAPPGTHAFYCHGCECFPLADHLNLTNHAIVQTLVNSV-SK 352

QY 281 TPPSCCVPTKLTPISILYIDAGNNVYKQYEDMVVESC GC 321

Db 353 IPKACCVPTLSALSMYLDENKVKLVKNYODMVVESC GC 393

RESULT 14

149541

bone morphogenetic protein 4 - mouse

C:Species: Mus musculus (house mouse)

Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999

Accession: 149541; S29523; B34201

R:Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; M

J. Biol. Chem. 270, 28364-28373, 1995

A:Title: The mouse bone morphogenetic protein-4 (BMP4) gene: Analysis of promoter util

Search completed: October 3, 2002, 15:39:45
Job time: 181 sec

Search completed: October 3, 2002, 15:39:45
Job time: 181 sec

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1368	77.9	436	1	GDF6_BOVIN	P55106	bos taurus
2	771	43.9	501	1	GDF5_HUMAN	P43026	homo sapiens
3	765	43.5	495	1	GDF5_MOUSE	P43027	mus musculus
4	691	39.3	125	1	GDF6_MOUSE	P43028	mus musculus
5	549	31.2	151	1	GDF7_MOUSE	P43029	mus musculus
6	426.5	24.3	398	1	BMF4_XENLA	P25703	xenopus laevis
7	426.5	24.3	398	1	BMF4_XENLA	P30884	xenopus laevis
8	418.5	23.8	405	1	BMF4_CHICK	Q90752	gallus gallus
9	406.5	23.1	408	1	BMF4_HUMAN	P12644	homo sapiens
10	405.5	23.1	452	1	BMF5_MOUSE	P49003	mus musculus
11	405.5	23.1	461	1	DVRL_STRPUB	P48969	strongyloides
12	403.5	23.0	395	1	BMF2_RABIT	O46564	oryctolagus
13	401	22.8	393	1	BMF2_RAT	P49001	rattus norvegicus
14	401	22.8	408	1	BMF4_MOUSE	P21275	mus musculus
15	398.5	22.7	409	1	BMF4_RABIT	O46576	oryctolagus
16	396.5	22.6	454	1	BMF5_HUMAN	P22003	homo sapiens
17	386	22.5	408	1	BMF4_RAT	Q06826	rattus norvegicus
18	395	22.5	394	1	BMF2_MOUSE	P21274	mus musculus
19	392.5	22.3	396	1	BMF2_DAMDA	O19006	dama dama
20	388.5	22.1	396	1	BMF2_HUMAN	P12643	homo sapiens
21	386	22.0	430	1	BMF7_MOUSE	P23359	mus musculus
22	386	22.0	431	1	BMF7_HUMAN	P18075	homo sapiens
23	385.5	21.9	402	1	BMF8_HUMAN	P34820	homo sapiens
24	384	21.9	426	1	BMF7_XENLA	P30886	xenopus laevis
25	382.5	21.8	399	1	BMF4_MOUSE	P34821	mus musculus
26	380	21.6	424	1	BM10_HUMAN	O95393	homo sapiens
27	378	21.5	408	1	BMF4_DAMDA	Q29607	dama dama
28	377	21.5	401	1	BMF4_XENLA	P30885	xenopus laevis
29	375	21.3	353	1	BMF2_CHICK	Q90751	gallus gallus
30	372	21.2	420	1	BM10_MOUSE	P91229	mus musculus
31	371.5	21.1	621	1	DECA_DROPS	P91699	drosophila
32	369	21.0	588	1	DECA_DROME	P07713	drosophila
33	369	21.0	593	1	DECA_DROME	P91706	drosophila

RESULT	1
GDF6_BOVIN	
ID	PRT; 436 AA.
P5106;	
AC	
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived morphogenetic protein 2) (CDMP-2) (Fragment).
DE	GDF6 OR CDMP2.
GN	Bos taurus (Bovine).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Articular cartilage;
RX	MEDLINE=95050604; PubMed=7961761;
RA	Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P., Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RA	"Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.";
RT	J. Biol. Chem. 269:28227-28234(1994).
RL	-! SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC	-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	-----
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CC	-----
DR	EMBL; U13661; AAA61416.1; ..
DR	HSSP; P18075; LBMP.
DR	InterPro; IPR001839; TGF-beta.
DR	InterPro; IPR001111; TGFB-N.
DR	Pfam; PF00019; TGF-beta; 1.
DR	Pfam; PF00688; TGFB_propeptide; 1.
DR	ProDom; PD000357; TGF-beta; 1.
DR	SMART; SM00204; TGFB; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Growth factor; cytokine; Glycoprotein.
FT	NON_TER
FT	1
FT	<1 316 POTENTIAL.
FT	CHAIN
FT	317 436 GROWTH/DIFFERENTIATION FACTOR 6.
FT	DISULFID 335 401 BY SIMILARITY.
FT	DISULFID 364 433 BY SIMILARITY.
FT	DISULFID 368 435 BY SIMILARITY.
FT	DISULFID 400 400 INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD 27 27 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 89 89 N-LINKED (GLCNAC...) (POTENTIAL).
SO	SEQUENCE 436 AA; 47873 MW; B0688E12EF8AE91D CRC64;

Query Match 77.9%; Score 1368; DB 1; Length 436;
Best Local Similarity 81.7%; Pred. No. 8.6e-93;
Matches 268; Conservative 9; Mismatches 39; Indels 12; Gaps 6;

QY 3 DLSTPLRRKYLFDVSMLEKELGAEALRLFRQAPSPAGPPACPLHVLQVLPCLSPILL 62
DB 112 DLSTPLRRKYLFDVSMLEKELGAEALRLFRQAPSPAGPPACPLHVLQVLPCLSPILL 170
QY 63 LDARTLDPOGAPGAGVEFVDMGQHRQPKWQKLCLELRAAW-GELDAGAEARARAPQPOOP 121
DB 171 GSAEP-CPAGAPRGWEVDWGRGLRPQPKWQKLCLELRAAWGEGPCEADEARTPQPOOP 229
QY 122 PPDLSRLSGRRVRPPQERALLVWTRSORKNLFEMREQLGSA-EAAGPGAGAGSGW- 179
DB 230 PPDLSRLSGRRVRPPQERALLVWTRSORKNLFEMREQLGSAEYVVGPGGAGSGP 289
QY 180 -----PPPSGAPDARPWLSPGRRRRRTAFASRHCKRHKSLRCLSKKPLHVNFKELG 233
DB 290 PPDPPPPPPSGTDPAGLWSPSG-RRRTAFASRHCKRHKSLRCLSKKPLHVNFKELG 348
QY 234 WDWIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLT 293
DB 349 WDWIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLT 408
QY 294 ISILYIDAGNNVYKQYEDWVWESGCR 321
DB 409 ISILYIDAGNNVYNEEYVWVWESGCR 436

RESULT 2
GDF5_HUMAN STANDARD; PRT; 501 AA.
AC P43026; Q96SBI;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 5 precursor (GDF-5) (Cartilage-derived morphogenetic protein 1) (CDMP-1).
DE GDF5 OR CDMP1.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
Y MEDLINE=95071375; PubMed=7980526;
Hootten G., Neidhardt H., Jacobowsky B., Pohl J.;
"Cloning and expression of recombinant human growth/differentiation factor 5";
RL Biochem. Biophys. Res. Commun. 204:646-652(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P., Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
"Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.";
RL J. Biol. Chem. 269:28227-28234(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P., Dunn M.,

Query Match

43.9%; Score 771; DB 1; Length 501;

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Levasialho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McNurray A.A., Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams D.R., Beck S., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20";
Nature 414:865-871(2001).
CC -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING HUMAN EMBRYONIC DEVELOPMENT.
CC -!- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE METACARPALS, METATARSALS AND PHALANXES ARE PARTICULARLY SHORT. THE PHALANXES ARE ALMOST SQUARE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL; X80915; CAA56874.1; -;
DR EMBL; U13660; AAA57007.1; -;
DR EMBL; AL121586; CAB89416.1; -;
DR HSSP; PL2643; 3BMP.
DR MIM; 601146; -;
DR MIM; 201250; -;
DR MIM; 200700; -;
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 381 POTENTIAL.
FT CHAIN 382 501 GROWTH/DIFFERENTIATION FACTOR 5.
FT DISULFID 400 466 BY SIMILARITY.
FT DISULFID 429 498 BY SIMILARITY.
FT DISULFID 433 500 BY SIMILARITY.
FT DISULFID 465 465 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 189 189 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 38 38 T -> S (IN REF. 2).
FT CONFLICT 254 258 APGGG -> VPSR (IN REF. 2).
FT CONFLICT 276 276 S -> A (IN REF. 2).
FT CONFLICT 321 321 A -> T (IN REF. 2).
FT CONFLICT 384 384 L -> S (IN REF. 2).
SQ SEQUENCE 501 AA; 55410 MW; 37985F2D15C4F5EF CRC64;

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DR PRINTS; PRO0438; GFCYSKNOT.
DR Prodom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.
FT SIGNAL 1 27
FT PROPEP 28 375
FT CHAIN 376 495
FT DISULFID 394 460
FT DISULFID 423 492
FT DISULFID 427 494
FT DISULFID 459 495
FT CARBOHYD 183 183
FT VARIANT 98 98
SQ SEQUENCE 495 AA; 54885 MW; 54885 MW; CDD05DE48185D2E3 CRC64;

Query Match 43.5%; Score 765; DB 1; Length 495;
Best Local Similarity 50.5%; Pred. No. 7.9e-49;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

QY 9 LRROKLYFDVSMLSKEELVGAEIRLFQAP---SAPWPPAGPL-HVOLFPCLSL----P 60
DB 211 VRKQYVFDISAL-EKDGSLCAELRIILKKPLDVAKPAVPSGVRVAQLKLSGPCSGROPA 269

QY 61 LLLDARTLPDQAPGAGHEVEDVWQGLRH-OPWQKLCLELRAANGELDAGAEARARGPQ 119
DB 270 ALLDVRSY--PGLDGSQGEVEDIWKLFNFNKAQLCLELE-AW---ERGRA----- 315

QY 120 QPPPLDLSRGFGRVRPPQPARLLVPTRSQRNKL-PAEMREQIGLSAAAGPAGABEGS 178
DB 316 ---VDRLGLGFETARQVHEKALFLVFGRTKKRDLFENEIKARSGQDDKT----- 362

QY 179 WPPPSGADPARWLPSPGRRRRRTAFASRHGRHGKKSRLRCSKKPLHVNFKELGWDWMI 238
DB 363 -----VYELFSQ--RRRRAPLANRQGRKPSKNLKARCSRKALHVNFKDMGWDWMI 412

QY 239 IAPLEYEAYHCEGVCDFPLRSHLEPTNHAITOTLMSWDGCTPPSCCVKLTPTISILY 298
DB 413 IAPLEYEAFHCEGJCEFPRLRSHLEPTNHAIVTOLMSWDPESTPTCCVTRLSPISILF 472

QY 299 IDAGNNVYKQYEDWVWVSCGCR 321
DB 473 IDSANNVYKQYEDWVWVSCGCR 495

RESULT 4
GDF6_MOUSE
ID_GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN GDF6 OR GDF-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.E.; Huynh T.V.; Copeland N.G.; Jenkins N.A.; Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RL member of the TGF beta-superfamily."
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC EMBL; U08338; AAA18779.1; -
 DR HSSP; P12643; 3BMP.
 DR MGD; MGI:95689; Gdf6.
 DR InterPro; IPR001839; TGF-beta.
 DR Pfam; PF00019; TGF-beta; 1.
 DR ProDom; PD000357; TGF-beta; 1.
 DR SMART; SM00204; TGF-beta; 1.
 DR PROSITE; PS00250; TGF-beta; 1.
 DR Growth factor; Cytokine; Glycoprotein.
 KW NON_TER 1 1
 FT PROPEP <1 5
 FT CHAIN 6 125
 FT DISULFID 24 90
 FT DISULFID 53 122
 FT DISULFID 57 124
 FT DISULFID 89 89
 FT INTERCHAIN (BY SIMILARITY).
 T SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match 39.38; Score 691; DB 1; Length 125;
 Best Local Similarity 99.28; Pred. No. 4.9e-44;
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 197 RRRRTAFASRRGKRGKSKPLRVNFKELGWDWIIAPLEYAYHCEGVCDFF 256
 DB 1 RRRRTAFASRRGKRGKSKPLRVNFKELGWDWIIAPLEYAYHCEGVCDFF 60
 QY 257 LRSLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVYKQYEDMVVE 316
 DB 61 LRSLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVYKQYEDMVVE 120
 QY 317 SCGCR 321
 DB 121 SCGCR 125

RESULT 5
 ID GDF7_MOUSE STANDARD; PRT; 151 AA.
 AC P43029;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 T Growth/differentiation factor 7 precursor (GDF-7) (Fragment).
 UN GDF7 OR GDF-7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAUB/C; TISSUE=Liver;
 RX MEDLINE=94195427; PubMed=8145850;
 RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
 RA Lee S.-J.;
 RT "Limb alterations in brachypodism mice due to mutations in a new
 RT member of the TGF-beta-superfamily";
 RL Nature 368:639-643(1994).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
 CC EMBL; U08339; AAA18780.1; -
 DR HSSP; P12643; 3BMP.
 DR MGD; MGI:95690; Gdf7.
 DR InterPro; IPR001839; TGF-beta.
 DR Pfam; PF00019; TGF-beta; 1.
 DR ProDom; PD000357; TGF-beta; 1.
 DR SMART; SM00204; TGF-beta; 1.
 DR PROSITE; PS00250; TGF-beta; 1.
 DR Growth factor; Cytokine; Glycoprotein.
 KW NON_TER 1 1
 FT PROPEP <1 5
 FT CHAIN 6 151
 FT DISULFID 50 116
 FT DISULFID 79 148
 FT DISULFID 83 150
 FT DISULFID 115 115
 FT DOMAIN 1 5
 FT DOMAIN 16 41
 FT SEQUENCE 151 AA; 15697 MW; 0E496AACB5827759 CRC64;

Query Match 31.2%; Score 549; DB 1; Length 151;
 Best Local Similarity 59.5%; Pred. No. 1.3e-33;
 Matches 103; Conservative 13; Mismatches 35; Indels 22; Gaps 1;
 QY 149 RSQRKNLFAMREQLGSAEAGFCAGAGSWPPSPGADPARDPWLPSGRRRRRTAFASRH 208
 DB 1 RRRRTALACTRGAQSGGGGGGGGGGGGGGGA----- 38
 QY 209 GKRHGKSRURCSKKPLRVNFKELGWDWIIAPLEYAYHCEGVCDFFPLRSHLEPTNHAI 268
 DB 39 GRGHRGRGRSCRKSLHVDVKELGWDWIIAPLEYAYHCEGVCDFFPLRSHLEPTNHAI 98
 QY 269 IQTLNMSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVYKQYEDMVVEGCR 321
 DB 99 IQTLNMSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVYKQYEDMVVEGCR 151

RESULT 6
 ID BMPA_XENLA STANDARD; PRT; 398 AA.
 AC P25703;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 2-1 precursor (BMP-2-1).
 OS Xenopus laevis (African clawed frog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91274367; PubMed=2054389;
 RA Plessow S., Koester M., Knoechel W.;
 RT "cDNA sequence of Xenopus laevis bone morphogenetic protein 2
 RT (BMP-2).";
 RL Biochim. Biophys. Acta 1089:280-282(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92378616; PubMed=1510675;
 RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
 RT "Genes for bone morphogenetic proteins are differentially transcribed
 RT in early amphibian embryos";
 RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL: X55031; CAA38850.1; -;
 DR EMBL: X63424; CAA45018.1; -;
 DR PIR: S16244; S16244.
 DR PIR: JH0687; JH0687.
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00688; TGF-beta; 1.
 DR Pfam: PF00688; TGF-beta; 1.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 284 BONE MORPHOGENETIC PROTEIN 2-I.
 FT DISULFID 298 363 BY SIMILARITY.
 FT DISULFID 327 395 BY SIMILARITY.
 FT DISULFID 331 397 BY SIMILARITY.
 FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 7 7 S -> P (IN REF. 2).
 FT CONFLICT 16 16 V -> L (IN REF. 2).
 FT CONFLICT 233 233 N -> T (IN REF. 2).
 SQ SEQUENCE 398 AA; 45575 MW; 150AC64A47D2E15F CRC64;

Query Match 24.3%; Score 426.5; DB 1; Length 398;
 Best Local Similarity 31.5%; Pred. No. 2.8e-24;
 Matches 105; Conservative 51; Mismatches 88; Indels 89; Gaps 13;

QY 12 OKYLFDSVMSLSDKEELVGAELRFRQAPSWPGPPAGPLH-VQLFCLSP-----61

DB 132 QREFFNLSSIPNEELVTSALRIFREQVQEPFSDSKLHRINIYDIVKPAASRGV 191

QY 62 -LLDARTLDPOGAPPAGWVDFVQGL-----RHQPKWLCLLELAANGELDAGEA 115

DB 192 RLDTRLIHN-----ESKWSFDTVPATARIHAKQPNHGFVEV-----NHL 236

QY 116 RGPOQPPPPDLRSLSGFRVRP-----PQRALLVFTSRQKNLFAEMREQLGSA 170

QY 237 -NDKNVPKKHVR-----ISRLTPDKDNWQIRPLLVTFSD-----G 273

QY 171 PGAGAGSNPPPPGAPDARPLSPGRRRRRTAFASRHGRHKKSLR--CSKKPLHVN 228

DB 274 KHALH-----KROKROA-----RHQKRLKSSCRHPLYVD 306

QY 229 KRLGWDWIIAPLEYAYHCEGVDPLRSHLEPTNHAIIOTLMNSMDPGSTPPSCV 288

DB 307 FSDVGNDWIIAPPGYHAFYCHGECPPPLADHLNSTNHAIVQTLVNSVNT-NIPKAC 365

QY 289 YLTPISILYIDAGNNVYKQYEDMVVESCGR 321

DB 366 TELSALSMYLDENEKVKLVNQYDMVVEGCGCR 398

RESULT 7

ID BMPB XENLA STANDARD; PRT; 398 AA.

AC P30884;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bone morphogenetic protein 2-II precursor (BMP-2-II).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92378616; PubMed=1510675;

RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;

RT "Genes for bone morphogenetic proteins are differentially transcribed

in early amphibian embryos.";

RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).

CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: X63425; CAA45019.1; -;
 DR PIR: JH0688; JH0688.
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-beta; 1.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 284 BONE MORPHOGENETIC PROTEIN 2-II.
 FT DISULFID 298 363 BY SIMILARITY.
 FT DISULFID 327 395 BY SIMILARITY.
 FT DISULFID 331 397 BY SIMILARITY.
 FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 398 AA; 45616 MW; 60E41FA2C8E603DC CRC64;

Query Match 24.3%; Score 426.5; DB 1; Length 398;
 Best Local Similarity 31.3%; Pred. No. 2.8e-24;
 Matches 104; Conservative 51; Mismatches 90; Indels 87; Gaps 12;

QY 12 OKYLFDSVMSLSDKEELVGAELRFRQAPSWPGPPAGPLH-VQLFCLSP-----61

DB 132 QREFFNLSSIPNEELVTSALRIFREQVQEPFSDSKLHRINIYDIVKPAASRGV 191

QY 62 -LLDARTLDPOGAPPAGWVDFVQGL-----RHQPKWLCLLELAANGELDAGEA 115

DB 192 RLDTRLIHN-----ESKWSFDTVPATARIHAKQPNHGFVEV-----NHL 248

QY 116 RGPOQPPPPDLRSLSGFRVRP-----PQRALLVFTSRQKNLFAEMREQLGSA 171

DB 249 S-----RSLTLDKHWPRIP-----LLVTFSD-----GK 274

QY 172 GAGAGSNPPPPGAPDARPLSPGRRRRRTAFASRHGRHKKSLR--CSKKPLHVN 229

DB 275 KHALH-----KROKROA-----RHQKRLKSSCRHPLYVD 307

QY 230 KRLGWDWIIAPLEYAYHCEGVDPLRSHLEPTNHAIIOTLMNSMDPGSTPPSCV 289

DB 308 FSDVGNDWIIAPPGYHAFYCHGECPPPLADHLNSTNHAIVQTLVNSVNT-NIPKAC 366

QY 290 YLTPISILYIDAGNNVYKQYEDMVVESCGR 321

Qy	121	PPPDLSRLSGRRVRRPQERALLVVFTRSQ-----RKNLFAEMREQUGSAAAGP	171
Db	284	--PTDAGVGVGN--NEGEPFVWFQRMEEVIATNSHLRRNRAATQKKG-----	332
Qy	172	GAGAECSWPPPSGADARPMLPSPGRRRR---TAFASRHCRHGKSKRLCSKKPLHV	227
Db	333	-----GKPRKPTDNDIASR-DSASSLNSDWQCRKNLFV	367
Qy	228	NFKELGWDDWIITAPLEYEAYHCEGVCDFPPLSHLEPTNHAIQTLLMSMDPGSTPPSCCV	287
Db	368	NEEDLDQEWIITAPLGYYAFYCQCEAFPLNGHANATNHAIVQTLVHHMSPSHVQPCCA	427
Qy	288	PKLPLPISILYIDAGNNVVYKQYEDMWVESCGC	320
Db	428	PKLPSPTIYLYDDSRNVVLLKKYKNMVRACGC	450

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RESULT 12
BMP2_RABIT
ID BMP2_RABIT STANDARD; PRT; 395 AA.
AC O46564;
DT DT
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2).
GN BMP2 OR BMP-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Ocular ciliary epithelium;
RC Wan X.L., Sears J., Chen S., Sears M.;
RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
RT epithelium";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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```

KW		SIGNAL; Growth factor;	Bone; Cartilage; Glycoprotein.
FT	1	POTENTIAL.	
FT	23	SIGNAL	
FT	PROPEP	24	BY SIMILARITY.
FT	CHAIN	281	BONE MORPHOGENETIC PROTEIN 2.
FT	DISULFID	395	BY SIMILARITY.
FT	DISULFID	295	BY SIMILARITY.
FT	DISULFID	360	BY SIMILARITY.
FT	DISULFID	324	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	324	N-LINKED (GLCNAC. .)
FT	DISULFID	378	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	DISULFID	359	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	359	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	134	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	199	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	337	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	337	SEQUENCE
FT	SEQUENCE	395 AA:	44664 MW; 8D1DDCFGAA582496 CRC64;
SQ			

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Query Match 23.0%; Score 403.5; DB 1; Length 395;
Best Local Similarity 30.5%; Pred. No. 1.3e-22;
Matches 100; Conservative 51; Mismatches 98; Indels 79; Gaps 12;

QY 12 QKYLFDVSMLSKDEELVGAELRQAPSPAGPLH-VQLPCLSP----- 61
DB 129 RRFNLTSTIPPEFTLSAELQVFEQMEALGDDSGFHRINIYEIIPATANSKFPAT 188
QY 62 -LLDARTLDPOGAPAGVDFVWGLRQHPWKQLCLLELRANGELDAEARGPQQ 120
DB 189 RLIDTRLVQN---TSRMESFDVTPAVMR--W-----TAQGHANHFV-VEVTHLEE 234
QY 121 PPPDLRSLGFGRRVP-----PQERALLVFTSRQKNLFAEMREQLGSAAAGPAGA 175
DB 235 KQGVSKRHVRISLHSLHDEHSQIRPLLVTE-----GH 268
QY 176 EGSWPPSGAPDAPWLPSPGRRRTAFASRHGRKHKSLR--CSKKPLHVNFKELG 233
DB 269 DKGEPHLH-----RREKQA-----KHKRKLKSSCKRHPLYVDFSDVG 308
QY 234 WDDTIIAPLEYEAYHCEGVCDPLSLHLEPTNHAIIQTLNMSMDPGSPCCVPTKLT 293
DB 309 WNDMIVAPCYHAFYCHGCEPPLADHLNSTNHAIVQTLVNSV-SKIPKACCVPTLSA 367
QY 294 ISLIIIDAGNNVYKQYEDMVVSGCGR 321
DB 368 ISMLTDEMEKVKLVKNYODMVVSGCGR 395

RESULT 13
BMP2_RAT ID BMP2_RAT STANDARD; PRT; 393 AA.
AC P49001;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z25868; CAA81088.1;
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
```

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FT PROPEP 20 279
FT CHAIN 280 393 BONE MORPHOGENETIC PROTEIN 2.
FT DISULFID 323 358 BY SIMILARITY.
FT DISULFID 322 390 BY SIMILARITY.
FT DISULFID 326 392 BY SIMILARITY.
FT DISULFID 337 357 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 393 AA; 44383 MW; 7D20865852E0F213 CRC64;

Query Match 22.8%; Score 401; DB 1; Length 393;
Best Local Similarity 30.8%; Pred. No. 2e-22;
Matches 105; Conservative 50; Mismatches 98; Indels 88; Gaps 13;

QY 2 SLSHTPLRROKYLFVSMLSKDEELVGAELRQAPSPAGPLHVLVOLPCLSP 61
DB 120 SEMSGKTSRR--FFENLSSVPTDFLTSAELQVFEQMEALGNSFQHRINIYEIIPKA 177
QY 62 -----LLDARTLDPOGAPAGVDFVWGLRQHPWKQLCLLELRANGELDAGEA 111
DB 178 TASSKFPVTRLEDTRLVTQN---TSQWESFDVTPAVMR--W-----TAQGHANHFV 224
QY 112 EARARGPOPPPPDLRSLGFGRRVRPQOERALLVFTSRQKNLFAEMREQLGSAAAGP 171
DB 225 VEVAHLEKPP-----GVSKR-----HVRISRLHQD----- 250
QY 172 GAGAECSWPPSGAPDAPWLPSPG-----RRRTAFASRHGRKHKSLR--C 220
DB 251 ----EHSW-----SQVRPLLVTFCHDGKGPLHKKRQA-----KHKRKLKSSC 293
QY 221 SKKPLHVNFKELGDDWIIAPLEYEAYHCEGVCDPLSLHLEPTNHAIIQTLNMSMDPGS 280
DB 294 KRHPLYYDFSDVGNWDWIVAPPGYHAFYCHGCEPPLADHLNSTNHAIVQTLVNSV-SK 352
QY 281 TPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVSGCGR 321
DB 353 IPKACCVPTLSAISMLYLDENEKVKLVKNYODMVVSGCGR 393

RESULT 14
BMP4_MOUSE ID BMP4_MOUSE STANDARD; PRT; 408 AA.
AC P21275;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B).
GN BMP4 OR BMP-4 OR DVR-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93282803; PubMed=8507180;
RA Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
RT "Murine bone morphogenetic protein-4 gene: existence of multiple
RL promoters and exons for the 5'-untranslated region.";
RL Biochem. Biophys. Res. Commun. 192:1049-1056(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93365172; PubMed=8358941;
RA Takaoka K., Yoshikawa H., Hasimoto J., Masuhara K., Miyamoto S.,
RA Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.;
RT "Gene cloning and expression of a bone morphogenetic protein derived
RT from a murine osteosarcoma.";
```


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OM protein - protein search, using sw model

Run on: October 3, 2002, 15:45:36 ; Search time 48.58 Seconds
(without alignments)
1143.091 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDLSHPTLRQKYLFDVSM.....GNVVYKQEDMVVSCGCR 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

al number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTEMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1000.5	56.9	399	13 Q9W753	Q9W753 xenopus lae
2	907	51.6	412	13 O12938	O12938 brachydanio
3	796	45.3	447	6 Q9BDW8	Q9BDW8 cercopithec
4	782	44.5	413	13 Q9DGN4	Q9DGN4 xenopus lae
5	771	43.9	501	4 Q96SBI	Q96SBI homo sapien
6	756	43.0	500	13 Q9W6G0	Q9W6G0 gallus gall
7	737	41.9	294	6 Q9BDW9	Q9BDW9 macaca fasc
8	712	40.5	324	13 Q9YHW9	Q9YHW9 gallus gall
9	698.5	39.8	261	13 Q9W6C0	Q9W6C0 brachydanio
10	664.5	37.8	257	13 O42303	O42303 brachydanio
11	634	36.1	441	11 Q99MV1	Q99MV1 mus musculu
12	612.5	34.9	126	13 Q93573	Q93573 gallus gall
13	451	25.7	277	13 Q90Y82	Q90Y82 lampetra ja
14	427.5	24.3	417	5 Q9XYQ7	Q9XYQ7 lytechinus
15	426	24.2	289	5 Q9XYQ8	Q9XYQ8 strongyloce
16	423.5	24.1	398	13 Q90YD7	Q90YD7 xenopus tro

17	408	23.2	400	13	O57574	O57574 brachydanio
18	406	23.1	400	13	O13107	O13107 brachydanio
19	405	23.1	364	13	Q9PWK1	Q9PWK1 gallus gall
20	405	23.1	391	13	O90YJ3	O90YJ3 brachydanio
21	402	22.9	301	5	O97390	O97390 crassostrea
22	401.5	22.9	204	5	Q9XZ69	Q9XZ69 tripneustes
23	400.5	22.8	337	6	Q9M2V5	Q9M2V5 canis famil
24	400	22.8	405	5	Q9U5E8	Q9U5E8 psychodera
25	399	22.7	361	5	O96504	O96504 brachiosteo
26	399	22.7	453	13	P87373	P87373 gallus gall
27	396.5	22.6	411	5	Q9U418	Q9U418 brachiosteo
28	390.5	22.2	128	5	O95W38	O95W38 schistocerc
29	389	22.1	432	13	Q9PTF9	Q9PTF9 brachydanio
30	387	22.0	390	13	Q91597	Q91597 xenopus lae
31	386.5	22.0	411	13	O93369	O93369 brachydanio
32	386	22.0	430	11	O91XF7	O91XF7 mus musculu
33	385.5	21.9	182	13	O90Y81	O90Y81 lampetra ja
34	385.5	21.9	191	5	O26468	O26468 schistocerc
35	384	21.9	313	13	O91403	O91403 gallus gall
36	384	21.9	398	13	O918T6	O918T6 gallus gall
37	381	21.7	614	5	P91720	P91720 drosophila
38	380.5	21.7	178	5	Q25211	Q25211 junonia coe
39	380.5	21.7	411	13	O57573	O57573 brachydanio
40	380	21.6	400	13	O73818	O73818 xenopus lae
41	379	21.6	400	13	O91703	O91703 xenopus lae
42	377.5	21.5	443	5	O76851	O76851 halocynthia
43	374.5	21.3	386	13	O13109	O13109 brachydanio
44	374	21.3	400	13	O90XD6	O90XD6 xenopus tro
45	369	21.0	588	5	O9VQC6	O9VQC6 drosophila

ALIGNMENTS

RESULT 1

Q9W753					
ID	Q9W753	PRELIMINARY:	PRT:	399	AA.
AC	O9W753:				
DT	01-NOV-1999 (TRENBLrel. 12, Created)				
DT	01-NOV-1999 (TRENBLrel. 12, Last sequence update)				
DT	01-DEC-2001 (TRENBLrel. 19, Last annotation update)				
DE	GROWTH AND DIFFERENTIATION FACTOR 6.				
GN	GDF6.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipelidae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99396700; PubMed=10393114;				
RA	Chang C., Hemmati-Brivanlou A.;				
RT	"Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.;"				
RL	Development 126:3347-3357(1999).				
CC	!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
DR	EMBL; AF155125; AAD38402.1; .				
DR	HSSP: P12643; 3BMP.				
DR	InterPro: IPR002405; Inhibin_alpha.				
DR	InterPro: IPR001839; TGF-beta.				
DR	InterPro: IPR001111; TGFb_N.				
DR	Pfam: PF00019; TGF-beta; 1.				
DR	Pfam: PF00688; TGFb_propeptide; 1.				
DR	PRINTS: PR000669; INHIBIN.				
DR	ProDom: PD000357; TGF-beta; 1.				
DR	SMART: SM00204; TGFb; 1.				
DR	PROSITE: PS00250; TGF_BETA; 1.				
KW	Glycoprotein.				
SQ	SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;				

Query Match 56.9%; Score 1000.5; DB 13; Length 399;
Best Local Similarity 63.9%; Pred. No. 2.7e-79;
Matches 205; Conservative 29; Mismatches 54; Indels 33; Gaps 5;

Qy	230	KELGWDWHIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPT	289
Db	322	KELGWDWHIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPESTPPSCCVPS	381
Qy	290	KLTPISILYIDAGNNVYKQYEDMVVESCGR	321
Db	382	KLSPISILYIDSGNNVYKQYEDMVVESCGR	413
RESULT	5		
Q96SB1	ID	Q96SB1	PRELIMINARY; PRT; 501 AA.
AC	Q96SB1;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	DJ47704.7 (GROWTH DIFFERENTIATION FACTOR 5 (CARTILAGE-DERIVED MORPHOGENETIC PROTEIN-1)).		
DE	GDF5.		
GN	OS Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Brown A.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL121586; CAB89416.1; .		
SQ	SEQUENCE 501 AA; 55410 MW; 37985F2D15C4F5EF CRC64;		
Query Match	43.9%; Score 771; DB 4; Length 501;		
Best Local Similarity	51.1%; Pred. No. 3.7e-59;		
Matches	166; Conservative 46; Mismatches 61; Indels 52; Gaps		
Qy	9	LRRQKYLFDYSMLSDKEELVCAELRLRQAPS-----APWPPAGPLHVQLFPCLS---59	
Db	217	VRKORYVFDISAL-EKDLGLGAELRIURKPSDTAKPAAPGGRAAQL---KLSCPSGRQ 273	
Qy	60	-PLLLDARTDPOCAPAGVEVDVMOGLRH-QPWKQCLLELRAANGELDAGAEARAG 117	
Db	274	PASLLDVRV--PGLDSGWEVDIWKLFNFKNQAQLCLELE-AW---ERGRA-----321	
Qy	118	PQPPPPDLRLSLGRRVRPPQERALLVYTRSORKNL-FAENRQOLGSAEAGPGAGAE 176	
Db	322	-----VDLRGLGFDRAARQVHEKALFLVFGTKKRLDFEIKARSGQDDKT-----368	
Qy	177	GSWPPSPGADPARWLSPGRRRRRTAFASRHGRHCKKSLRCSKKPLHVNFKELGWD 236	
Db	369	-----VYELFSQ-RRKRAPLATRQGRKPSKNLKARCSKKALHVNFKDMGWD 416	
Qy	237	WIAPLEYAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 296	
Db	417	WIAPLEYAYHCEGLCEFFPLRSHLEPTNHAIQTLMNSMDPESTPTCCVPTRLSPIS 476	
Qy	297	LYIDAGNNVYKQYEDMVVESCGR 321	
Db	477	LFIDSANNVYKQYEDMVVESCGR 501	
RESULT	6		
Q9W6G0	ID	Q9W6G0	PRELIMINARY; PRT; 500 AA.
AC	Q9W6G0;		
DT	01-NOV-1999 (TrEMBLrel. 12, Created)		
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)		
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	GDF-5 PROTEIN.		
GN	GDF5.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		

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OX NCBI_TaxID=9031;
RN [ ]
RP SEQUENCE FROM N.A.
RX MEDLINE=99146893; PubMed=10021348;
RA Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,
RL Ladhler R., Allen S., Macpherson S., Luyten F.P., Archer C.W.;
RT "Mechanisms of GDF-5 action during skeletal development.";
RC Development 126:1305-1315(1999).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR ENBL; AF123389; AAD30451.1; -.
DS HSPG; P12643; BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFB_N.
DR Pfam: PF000019; TGF-beta; 1.
DR PRINTS: PR00669; INHIBIN.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00304; TGFB; 1..
DR PROSITE: PS002250; TGF_BETA; 1.
RS Glycoprotein.
} SEQUENCE 500 AA; 55952 MW; 1DE8385A3119A598 CRC64;

Query Match      43.0%; Score 756; DB 13; Length 500;
Best Local Similarity 49.5%; Pred.No.7.4e-59;
Matches 159; Conservative 47; Mismatches 69; Indels 46; Gaps 10;

QY   9 LRROKYLFDVSMLSDKELYCAELRFRQAPSAPWGPAG--PLHVQLFPC-----LSPLL 62
Db    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY  218 IRKOYIFDYSAL-EKDGLIVAEIIRUKNPSTDWKSHSGKTSOVKLFSCSTNRQAATL 276
Db    |||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY   63 LDARTLDPOGAAPPAGWGVVDVWGOLRH-QPWKLQCLLELRAAWGEILDAGEAEARAARGPQP 121
Db    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  277 LDSRTVSITDPK--WEVFDIWLKFNFKNLVNLCFELET----FDRGRA----- 320
Db    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  122 PPDLRSLGCGRRVRPPQRERALLVVFTSRKKNI-FAMREQLGSABAAGPGAGAEGSWP 180
Db    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  321 --VDLTRVGFNRTGRQYNRKALFLVFGTRTKRDLPFFNEIKARSQQDKT----- 367
Db    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  181 PSPGAPDAWPWPSGRRRRRTAFASRGHRGGKSKRLCKSKPLHVNFKELGWDDIIIA 240
Db    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  368 -----VVEYLFNQ-RKRRAPLATQGGRPKSNLKRPCRSKRALHNFKDMGDWDIIIA 419
Db    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  241 PLEYAYHCBCVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISILIYD 300
Db    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY  420 PLEYEAYHCBCFCPEPLRSHLEPTNHAVIQTLNMNSMDESTPTTCVPCTRLSPIILFID 479
Db    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
'v     301 AGNNVTYKYEDMWVESCGCR 321
        : |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
        480 SANNVVYKYEDMWVESCGCR 500

RESULT 7
Q9BDW9 ID Q9BDW9 PRELIMINARY; PRT; 294 AA.
AC Q9BDW9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Carpopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [ ]
RP SEQUENCE FROM N.A.
RX TISSUE=CEREBRAL CORTEX MOTOR AREA;
RM MEDLINE=21136583; PubMed=11238730;
RA Watakabe A., Fujita H., Hayashi M., Yamamoto T.;
RT "growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex.";
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25

②

209

21

153

30

96

38

150

89

10

1

52

117

Matches 144; Conservative 32; Mismatches 53; Indels 49; Gaps 9;

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QY 52 VQLPPCLSL---PLLDARTLDPOGAPPAGWEVFDVW---QGLRHQFWKQLCLELRAANG 104
Db 21 LRLFTCASGKNAAVLLQARPDFSHSA--SYWEVFDIWKVKFNRP--QLCLELDA--- 73
QY 105 ELDAEAEARAGPQQPPPLDRLSLGFRVRPPOERALLVVFTRSORKNLF-AEMREOL 163
Db 74 -VDHGR-----PUDRLGLSLRAGROTKEKAFVVFVGRTKKRLGYNETKAR- 119
QY 164 GSAAAGPGAGAGSGWPPSPGADARPLWPSGRRRRRTAFASRHKGRKSLRSCSK 223
Db 120 -----SGHDKNTVYELVTFQRRMRRAPLPR-GKKPIKPKQRCNRK 159
QY 224 PLAVNFKELGWDWIIAPLEYEYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPP 283
Db 160 OLHVNFKEGWDWIIAPLEYEYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPRSTPP 219
QY 284 SCCVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 321
Db 220 TCCVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 257
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RESULT 11
Q99MY1
ID AC Q99MY1 PRELIMINARY; PRT; 441 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
GN GDF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT2;
RX MEDLINE=21136583; PubMed=11238730;
RA Wataabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RL primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF254571; AAK30843.1; -.
DR EMBL; AF254570; AAK30843.1; JOINED.
DR HSSP; PL2643; 3BMP.
DR InterPro; IPR002405; Inhibin.alpha.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR Glycoprotein.
FT NON_TER 441 441
SQ SEQUENCE 441 AA; 45617 MW; 74DA312A853701F0 CRC64;
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Query Match 36.1%; Score 634; DB 11; Length 441;
Best Local Similarity 44.5%; Pred. No. 2.8e-47;
Matches 153; Conservative 33; Mismatches 70; Indels 88; Gaps 13;
QY 12 QKYLEFVMSLSEKELVGAELRFRQAPSAP-----WGPPAGPLHVQLFP 56
Db 132 QSFLEFVMSLSEADEVYNAELVRLRRSPEDRDSATLLPRLSLSTCPDEAGTAH----- 186
QY 57 CLSPLLDARTLDPOGAPPAGWEVFDVWQGLR-HQPW-----KQLCLELRAANGELDAGEA 111
Db 187 -----LLHSRAAEPLGG--ARWEAFDVTDAVQSHRRPRASRKFCLVLR-----VTASES 235
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QY 112 EARARGPOPPPPDLRLSLGFG-----RRVRPPOERALLVVFTRSORKNLF-AEMREOLG 164
Db 236 S-----PLAIRRLGFGWPGCGGGGTAAERALLVVISSRTQRAKESLPREIRAQAR 285
QY 165 SAAAGPGAGAGSGWPPSPGADARPLWPS-PGRRRRRTAFASR- 208
Db 286 ALRAA-----AE---PPDPGPGAGSRKANLGGRRRRRTALAGTRGADGSGGGGGGGGG 337
QY 209 -----GKRHGKSLRSCSKKPLHVNFKELGWDWIIAPLEYEYHCEGVCDFPL 257
Db 338 GGGGGGGGGAGRGHRRGRSRKSLHVDKELGWDWIIAPLDY EAYHCEGVCDFPL 397
QY 258 RSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPIISILYIDA 301
Db 398 RSHLEPTNHAIIQTLNMSMDPAAPASCVCVPARLSPISILYIDA 441
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RESULT 12
O93573
ID AC O93573 PRELIMINARY; PRT; 126 AA.
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN GDF6/7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
RT of a discrete class of commissural interneurons in the mouse spinal
RT cord.";
RL Genes Dev. 12:3394-3407(1998).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF089086; AAC97113.1; -.
DR HSSP; PL2643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin.alpha.
DR InterPro; IPR001839; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR Glycoprotein.
FT NON_TER 1 1
SQ SEQUENCE 126 AA; 14265 MW; CB924D280F44A394 CRC64;
```

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Query Match 34.9%; Score 612.5; DB 13; Length 126;
Best Local Similarity 86.5%; Pred. No. 4.9e-46;
Matches 109; Conservative 10; Mismatches 6; Indels 1; Gaps 1;
QY 197 RRRRTAFASRHKGR-HGKRSRLRSCSKKPLHVNFKELGWDWIIAPLEYEYHCEGVCDF 255
Db 1 RRRRTTIAARSGRGHGKAKTRCSRKPLHVNFKELGWDWIIAPLDY EAYHCEGVCDF 60
QY 256 PLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVYKQYEDMV 315
Db 61 PLRSHLEPTNHAIIQTLNMSMDPESTPPSCCVPSKLSILYIDSGNVVYKQYEDMV 120
QY 316 ESCGR 321
Db 121 ETGCR 126
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RESULT 13
Q90Y82 ID Q90Y82 PRELIMINARY; PRT; 277 AA.
AC Q90Y82;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LJBM2/4A (FRAGMENT).
GN LJBM2/4A.
OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxID=94989;
RN [1]
RP SEQUENCE FROM N.A.
RA Shigetani Y., Sugahara F., Kawakami Y., Murakami Y., Hirano S.,
RA Kuratani S.;
RT "Shape precedes structure: an exaptation for the vertebrate jaw
evolution.";
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AB071890; BAB6395.1; -.
FT NON_TER 1
SQ SEQUENCE 277 AA; 30507 MW; 30FB94C547AD99B0 CRC64;

Query Match 25.7%; Score 451; DB 13; Length 277;
Best Local Similarity 34.5%; Pred. No. 1.5e-31;
Matches 112; Conservative 45; Mismatches 98; Indels 70; Gaps 13;

QY 19 SMLSDKEELVGAELRLFRQAPSNWPGPPAGPLH-VQLFCLSPILLD-----ARTLDPQ-- 71
Db 1 SSIPGGEVTSALHVLVIRERLS---GPARAALHRLNVYEVLPAAADGTPIALRLDTRV 57
QY 72 GAPPAGWEVFDV-----WQGLRHQPKWQCLCELAAGGELDAGAEARARGPQPPPPD 125
Db 58 HSGRSEMERFVSPAAVNAAR-APNHGLLVEVH-----HLDGGTPEKR----- 101
QY 126 LNSLGRVRVRPQERALLVTRSORKNLFAEMREQLGSAEAGAGAGAGSWPPPPGA 185
Db 102 -RHVRIGRSLH-----AEAVAAARDGAGEGGDG-----EGW 133
QY 186 PDARPWLPs---PGRRRRTAFASRGKRH-----GKSLRUCSKPLHVNFKELGWD 236
Db 134 POLRPLVTFGHDGKTRDGTLLRPRKNSRPNKGRGRCQARYPLVDFSDVGWND 193
QY 237 WIAPILEYAYHCEGVCDPPLRSHLEPTNHAIQTILMSMDGSPPPSCCVPTKLTPIS 296
Db 194 WIVAPPGYNAPFCQGCHEFLPQHLNSTNHAIVQTLVNSVNP-EVPRACCIPTLTPIAL 252
QY 297 LYIDAGNNVYKQYEDMNVESCGCR 321
Db 253 LYLDEYKVLKNYQDMVVEGCGCR 277

RESULT 14
Q9XYQ7 ID Q9XYQ7 PRELIMINARY; PRT; 417 AA.
AC Q9XYQ7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4.
GN BMP2/4.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;

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RT "A BMP pathway regulates cell fate allocation along the sea urchin
animal-vegetal embryonic axis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF119712; AAD28038.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00669; INHIBIN.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 417 AA; 47727 MW; 5EB93E3022BFC50F CRC64;

Query Match 24.3%; Score 427.5; DB 5; Length 417;
Best Local Similarity 31.5%; Pred. No. 2.7e-29;
Matches 108; Conservative 54; Mismatches 100; Indels 81; Gaps 11;

QY 7 TPLRRQKYLFDVSMLSDKKEELVGAELRLFR-----QAPSAPWGPAGPLH---VQ 53
Db 128 TEHRHTVIFNISTMPAEVEVLTMAELRFRKDLLEHSTAKRHALDDRKSLPIHIMORIN 187
QY 54 LFPCLSPIL-----LLDARTLDPOCAPAGWEVFDV-----WQGLRHQPKWQCLCE 98
Db 188 VFHILKPVARNRDTIKRLDTRLDVDRN---SSNESFDVRPAVTSWEV---PEKNHGLE 241
QY 99 LRAANGELDAGEAARARGPQPPPPDLRLSLGFGRRVRPPOERALLVTRSORKNLFAE 158
Db 242 I-----EL-----IDSRGR-----PSPNHHVVRVTRADPSKVQEL-----QNEEDERWFQ 282
QY 159 MREOLGSAEAGAGAGAGSWPPPSGADPARPWLPSGRRRRRTAFASRGKRHKKSKRL 218
Db 283 TRPQLVITYSDG-----RTKSPSRGKRKRKRLKA 314
QY 219 RCKSKPLHVNFKELGWDWIIAPLEYAYHCEGVCDPPLRSHLEPTNHAIQTILMSMDP 278
Db 315 NCRHRLPLVDFSDVHNDWIVAPAGYAYCHGECPPFLAEHLNTTNHAIQTLVNSVNP 374
QY 279 GSTPSCCVPTKLPISTILYIDAGNNVYKQYEDMNVESCGCR 321
Db 375 ALVPKACGCGPTLSAISMLYLDYKVLKNYQDMVVEGCGCR 417

RESULT 15
Q9XYQ8 ID Q9XYQ8 PRELIMINARY; PRT; 289 AA.
AC Q9XYQ8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4 (FRAGMENT).
GN BMP2/4.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;
RT "A BMP pathway regulates cell fate allocation along the sea urchin
animal-vegetal embryonic axis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF119713; AAD28039.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.

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Search completed: October 3, 2002, 15:45:37
Job time: 413 sec